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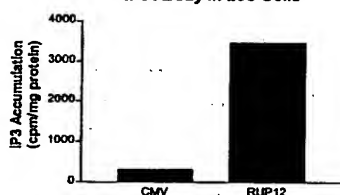
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(54) Title: ENDOGENOUS AND NON-ENDOGENOUS VERSIONS OF HUMAN G PROTEIN-COUPLED RECEPTORS

IP3 Assay in 293 Cells



(57) Abstract: The invention disclosed in this patent document relates to transmembrane receptors, more particularly to a human G protein-coupled receptor for which the endogenous ligand is unknown ("orphan GPCR receptors"), and most particularly to mutated (non-endogenous) versions of the human GPCRs for evidence of constitutive activity.

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ENDOGENOUS AND NON-ENDOGENOUS VERSIONS OF
HUMAN G PROTEIN-COUPLED RECEPTORS

FIELD OF THE INVENTION

The invention disclosed in this patent document relates to transmembrane receptors, and more particularly to human G protein-coupled receptors, and specifically to endogenous human GPCRs with particular emphasis on non-endogenous versions of the GPCRs that have been altered to establish or enhance constitutive activity of the receptor. Preferably, the altered GPCRs are used for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having potential applicability as therapeutic agents.

BACKGROUND OF THE INVENTION

Although a number of receptor classes exist in humans, by far the most abundant and therapeutically relevant is represented by the G protein-coupled receptor (GPCR or GPCRα) class. It is estimated that there are some 100,000 genes within the human genome, and of these, approximately 2%, or 2,000 genes, are estimated to code for GPCRs. Receptors, including GPCRs, for which the endogenous ligand has been identified are referred to as "known" receptors, while receptors for which the endogenous ligand has not been identified are referred to as "orphan" receptors. GPCRs represent an important area for the development of pharmaceutical products: from approximately 20 of the 100 known GPCRs, approximately 60% of all prescription pharmaceuticals have been developed.

GPCRs share a common structural motif. All these receptors have seven sequences of between 22 to 24 hydrophobic amino acids that form seven alpha helices, each of which spans the membrane (each span is identified by number, i.e., transmembrane-1 (TM-1), transmembrane-2 (TM-2), etc.). The transmembrane helices are joined by strands of amino acids between transmembrane-2 and transmembrane-3,

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transmembrane-4 and transmembrane-5, and transmembrane-6 and transmembrane-7 on the exterior, or "extracellular" side, of the cell membrane (these are referred to as "extracellular" regions 1, 2 and 3 (EC-1, EC-2 and EC-3), respectively). The transmembrane helices are also joined by strands of amino acids between transmembrane-1 and transmembrane-2, transmembrane-3 and transmembrane-4, and transmembrane-5 and transmembrane-6 on the interior, or "intracellular" side, of the cell membrane (these are referred to as "intracellular" regions 1, 2 and 3 (IC-1, IC-2 and IC-3), respectively). The "carboxy" ("C") terminus of the receptor lies in the intracellular space within the cell, and the "amino" ("N") terminus of the receptor lies in the extracellular space outside of the cell.

Generally, when an endogenous ligand binds with the receptor (often referred to as "activation" of the receptor), there is a change in the conformation of the intracellular region that allows for coupling between the intracellular region and an intracellular "G-protein." It has been reported that GPCRs are "promiscuous" with respect to G proteins, i.e., that a GPCR can interact with more than one G protein. See, Kenakin, T., *43 Life Sciences* 1095 (1988). Although other G proteins exist, currently, Gq, Gi, Gs and Go are G proteins that have been identified. Endogenous ligand-activated GPCR coupling with the G-protein begins a signaling cascade process (referred to as "signal transduction"). Under normal conditions, signal transduction ultimately results in cellular activation or cellular inhibition. It is thought that the IC-3 loop as well as the carboxy terminus of the receptor interact with the G protein.

Under physiological conditions, GPCRs exist in the cell membrane in equilibrium between two different conformations: an "inactive" state and an "active" state. A receptor in an inactive state is unable to link to the intracellular signaling transduction pathway to produce a biological response. Changing the receptor

conformation to the active state allows linkage to the transduction pathway (via the G-protein) and produces a biological response.

A receptor may be stabilized in an active state by an endogenous ligand or a compound such as a drug. Recent discoveries, including but not exclusively limited to modifications to the amino acid sequence of the receptor, provide means other than endogenous ligands or drugs to promote and stabilize the receptor in the active state conformation. These means effectively stabilize the receptor in an active state by simulating the effect of an endogenous ligand binding to the receptor. Stabilization by such ligand-independent means is termed "constitutive receptor activation."

SUMMARY OF THE INVENTION

Disclosed herein are endogenous and non-endogenous versions of human GPCRs and uses thereof.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 provides an illustration of second messenger IP₃ production from endogenous version RUP12 ("RUP12") as compared with the control ("CMV").

Figure 2 is a graphic representation of the results of a second messenger cell-based cyclic AMP assay providing comparative results for constitutive signaling of endogenous RUP13 ("RUP13") and a control vector ("CMV").

Figure 3 is a diagrammatic representation of the signal measured comparing CMV, endogenous RUP13 ("RUP13 wt") and non-endogenous, constitutively activated RUP13 ("RUP13(A268K)"), utilizing 8XCRE-Luc reporter plasmid.

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Figure 12 is a graphic representation of results from a primary screen of several candidate compounds against RUP13; results for "Compound A" are provided in well A2 and "Compound B" are provided in well G9.

DETAILED DESCRIPTION

The scientific literature that has evolved around receptors has adopted a number of terms to refer to ligands having various effects on receptors. For clarity and consistency, the following definitions will be used throughout this patent document. To the extent that these definitions conflict with other definitions for these terms, the following definitions shall control:

AGONISTS shall mean materials (e.g., ligands, candidate compounds) that activate the intracellular response when they bind to the receptor, or enhance GTP binding to membranes.

AMINO ACID ABBREVIATIONS used herein are set out in Table A:

TABLE A

ALANINE	ALA	A
ARGININE	ARG	R
ASPARAGINE	ASN	N
ASPARTIC ACID	ASP	D
CYSTEINE	CYS	C
GLUTAMIC ACID	GLU	E
GLUTAMINE	GLN	Q
GLYCINE	GLY	G
HISTIDINE	HIS	H
ISOLEUCINE	ILE	I
LEUCINE	LEU	L
LYSINE	LYS	K
METHIONINE	MET	M

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Figure 4 is a graphic representation of the results of a [³⁵S]GTPγS assay providing comparative results for constitutive signaling by RUP13:Gs Fusion Protein ("RUP13-Gs") and a control vector ("CMV").

Figure 5 is a diagrammatic representation of the signal measured comparing CMV, endogenous RUP14 ("RUP14 wt") and non-endogenous, constitutively activated RUP13 ("RUP14(L246K)"), utilizing 8XCRE-Luc reporter plasmid.

Figure 6 is a diagrammatic representation of the signal measured comparing CMV, endogenous RUP15 ("RUP15 wt") and non-endogenous, constitutively activated RUP15 ("RUP15(A398K)"), utilizing 8XCRE-Luc reporter plasmid.

Figure 7 is a graphic representation of the results of a second messenger cell-based cyclic AMP assay providing comparative results for constitutive signaling of endogenous RUP15 ("RUP15 wt"), non-endogenous, constitutively activated version of RUP15 ("RUP15(A398K)") and a control vector ("CMV").

Figure 8 is a graphic representation of the results of a [³⁵S]GTPγS assay providing comparative results for constitutive signaling by RUP15:Gs Fusion Protein ("RUP15-Gs") and a control vector ("CMV").

Figure 9 provides an illustration of second messenger IP₃ production from endogenous version RUP17 ("RUP17") as compared with the control ("CMV").

Figure 10 provides an illustration of second messenger IP₃ production from endogenous version RUP21 ("RUP21") as compared with the control ("CMV").

Figure 11 is a diagrammatic representation of the signal measured comparing CMV, endogenous RUP23 ("RUP23 wt") and non-endogenous, constitutively activated RUP23 ("RUP23(W275K)"), utilizing 8XCRE-Luc reporter plasmid.

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PHENYLALANINE	PHE	F
PROLINE	PRO	P
SERINE	SER	S
THREONINE	THR	T
TRYPTOPHAN	TRP	W
TYROSINE	TYR	Y
VALINE	VAL	V

PARTIAL AGONISTS shall mean materials (e.g., ligands, candidate compounds) that activate the intracellular response when they bind to the receptor to a lesser degree/extent than do agonists, or enhance GTP binding to membranes to a lesser degree/extent than do agonists.

ANTAGONIST shall mean materials (e.g., ligands, candidate compounds) that competitively bind to the receptor at the same site as the agonists but which do not activate the intracellular response initiated by the active form of the receptor, and can thereby inhibit the intracellular responses by agonists or partial agonists.

ANTAGONISTS do not diminish the baseline intracellular response in the absence of an agonist or partial agonist.

CANDIDATE COMPOUND shall mean a molecule (for example, and not limitation, a chemical compound) that is amenable to a screening technique. Preferably, the phrase "candidate compound" does not include compounds which were publicly known to be compounds selected from the group consisting of inverse agonist, agonist or antagonist to a receptor, as previously determined by an indirect identification process ("indirectly identified compound"); more preferably, not including an indirectly identified compound which has previously been determined to have therapeutic efficacy in at least one mammal; and, most preferably, not including an indirectly identified compound which has previously been determined to have therapeutic utility in humans.

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COMPOSITION means a material comprising at least one component; a "pharmaceutical composition" is an example of a composition.

COMPOUND EFFICACY shall mean a measurement of the ability of a compound to inhibit or stimulate receptor functionality, as opposed to receptor binding affinity. Exemplary means of detecting compound efficacy are disclosed in the Example section of this patent document.

CODON shall mean a grouping of three nucleotides (or equivalents to nucleotides) which generally comprise a nucleoside (adenosine (A), guanosine (G), cytidine (C), uridine (U) and thymidine (T)) coupled to a phosphate group and which, when translated, encodes an amino acid.

CONSTITUTIVELY ACTIVATED RECEPTOR shall mean a receptor subject to constitutive receptor activation. A constitutively activated receptor can be endogenous or non-endogenous.

CONSTITUTIVE RECEPTOR ACTIVATION shall mean stabilization of a receptor in the active state by means other than binding of the receptor with its endogenous ligand or a chemical equivalent thereof.

CONTACT or **CONTACTING** shall mean bringing at least two moieties together, whether in an in vitro system or an in vivo system.

DIRECTLY IDENTIFYING or **DIRECTLY IDENTIFIED**, in relationship to the phrase "candidate compound", shall mean the screening of a candidate compound against a constitutively activated receptor, preferably a constitutively activated orphan receptor, and most preferably against a constitutively activated G protein-coupled cell surface orphan receptor, and assessing the compound efficacy of such compound. This phrase is, under no circumstances, to be interpreted or understood to be encompassed by or to encompass the phrase "indirectly identifying" or "indirectly identified."

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protein can be fused directly to the c-terminus of the constitutively active GPCR or there may be spacers between the two.

HOST CELL shall mean a cell capable of having a Plasmid and/or Vector incorporated therein. In the case of a prokaryotic Host Cell, a Plasmid is typically replicated as an autonomous molecule as the Host Cell replicates (generally, the Plasmid is thereafter isolated for introduction into a eukaryotic Host Cell); in the case of a eukaryotic Host Cell, a Plasmid is integrated into the cellular DNA of the Host Cell such that when the eukaryotic Host Cell replicates, the Plasmid replicates. Preferably, for the purposes of the invention disclosed herein, the Host Cell is eukaryotic, more preferably, mammalian, and most preferably selected from the group consisting of 293, 293T and COS-7 cells.

INDIRECTLY IDENTIFYING or **INDIRECTLY IDENTIFIED** means the traditional approach to the drug discovery process involving identification of an endogenous ligand specific for an endogenous receptor, screening of candidate compounds against the receptor for determination of those which interfere and/or compete with the ligand-receptor interaction, and assessing the efficacy of the compound for affecting at least one second messenger pathway associated with the activated receptor.

INHIBIT or **INHIBITING**, in relationship to the term "response" shall mean that a response is decreased or prevented in the presence of a compound as opposed to in the absence of the compound.

INVERSE AGONISTS shall mean materials (e.g., ligand, candidate compound) which bind to either the endogenous form of the receptor or to the constitutively activated form of the receptor, and which inhibit the baseline intracellular response initiated by the active form of the receptor below the normal base level of activity which

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ENDOGENOUS shall mean a material that a mammal naturally produces.

ENDOGENOUS in reference to, for example and not limitation, the term "receptor," shall mean that which is naturally produced by a mammal (for example, and not limitation, a human) or a virus. By contrast, the term **NON-ENDOGENOUS** in this context shall mean that which is not naturally produced by a mammal (for example, and not limitation, a human) or a virus. For example, and not limitation, a receptor which is not constitutively active in its endogenous form, but when manipulated becomes constitutively active, is most preferably referred to herein as a "non-endogenous, constitutively activated receptor." Both terms can be utilized to describe both "in vivo" and "in vitro" systems. For example, and not limitation, in a screening approach, the endogenous or non-endogenous receptor may be in reference to an in vitro screening system. As a further example and not limitation, where the genome of a mammal has been manipulated to include a non-endogenous constitutively activated receptor, screening of a candidate compound by means of an in vivo system is viable.

G PROTEIN COUPLED RECEPTOR FUSION PROTEIN and **GPCR FUSION PROTEIN**, in the context of the invention disclosed herein, each mean a non-endogenous protein comprising an endogenous, constitutively activate GPCR or a non-endogenous, constitutively activated GPCR fused to at least one G protein, most preferably the alpha (α) subunit of such G protein (this being the subunit that binds GTP), with the G protein preferably being of the same type as the G protein that naturally couples with endogenous orphan GPCR. For example, and not limitation, in an endogenous state, if the G protein "G α " is the predominate G protein that couples with the GPCR, a GPCR Fusion Protein based upon the specific GPCR would be a non-endogenous protein comprising the GPCR fused to G α ; in some circumstances, as will be set forth below, a non-predominant G protein can be fused to the GPCR. The G

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is observed in the absence of agonists or partial agonists, or decrease GTP binding to membranes. Preferably, the baseline intracellular response is inhibited in the presence of the inverse agonist by at least 30%, more preferably by at least 50%, and most preferably by at least 75%, as compared with the baseline response in the absence of the inverse agonist.

KNOWN RECEPTOR shall mean an endogenous receptor for which the endogenous ligand specific for that receptor has been identified.

LIGAND shall mean an endogenous, naturally occurring molecule specific for an endogenous, naturally occurring receptor.

MUTANT or **MUTATION** in reference to an endogenous receptor's nucleic acid and/or amino acid sequence shall mean a specified change or changes to such endogenous sequences such that a mutated form of an endogenous, non-constitutively activated receptor evidences constitutive activation of the receptor. In terms of equivalents to specific sequences, a subsequent mutated form of a human receptor is considered to be equivalent to a first mutation of the human receptor if (a) the level of constitutive activation of the subsequent mutated form of a human receptor is substantially the same as that evidenced by the first mutation of the receptor; and (b) the percent sequence (amino acid and/or nucleic acid) homology between the subsequent mutated form of the receptor and the first mutation of the receptor is at least about 80%, more preferably at least about 90% and most preferably at least 95%. Ideally, and owing to the fact that the most preferred cassettes disclosed herein for achieving constitutive activation includes a single amino acid and/or codon change between the endogenous and the non-endogenous forms of the GPCR, the percent sequence homology should be at least 98%.

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NON-ORPHAN RECEPTOR shall mean an endogenous naturally occurring molecule specific for an endogenous naturally occurring ligand wherein the binding of a ligand to a receptor activates an intracellular signaling pathway.

ORPHAN RECEPTOR shall mean an endogenous receptor for which the endogenous ligand specific for that receptor has not been identified or is not known.

PHARMACEUTICAL COMPOSITION shall mean a composition comprising at least one active ingredient, whereby the composition is amenable to investigation for a specified, efficacious outcome in a mammal (for example, and not limitation, a human). Those of ordinary skill in the art will understand and appreciate the techniques appropriate for determining whether an active ingredient has a desired efficacious outcome based upon the needs of the artisan.

PLASMID shall mean the combination of a Vector and cDNA. Generally, a Plasmid is introduced into a Host Cell for the purposes of replication and/or expression of the cDNA as a protein.

SECOND MESSENGER shall mean an intracellular response produced as a result of receptor activation. A second messenger can include, for example, inositol triphosphate (IP₃), diacylglycerol (DAG), cyclic AMP (cAMP), and cyclic GMP (cGMP). Second messenger response can be measured for a determination of receptor activation. In addition, second messenger response can be measured for the direct identification of candidate compounds, including for example, inverse agonists, agonists, partial agonists and antagonists.

STIMULATE or STIMULATING, in relationship to the term "response" shall mean that a response is increased in the presence of a compound as opposed to in the absence of the compound.

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The efforts of the Human Genome project has led to the identification of a plethora of information regarding nucleic acid sequences located within the human genome; it has been the case in this endeavor that genetic sequence information has been made available without an understanding or recognition as to whether or not any particular genomic sequence does or may contain open-reading frame information that translate human proteins. Several methods of identifying nucleic acid sequences within the human genome are within the purview of those having ordinary skill in the art. For example, and not limitation, a variety of human GPCRs, disclosed herein, were discovered by reviewing the GenBank™ database. Table B, below, lists several endogenous GPCRs that we have discovered, along with other GPCR's that are homologous to the disclosed GPCR.

TABLE B

Disclosed Human Orphan GPCRs	Accession Number Identified	Open Reading Frame (Base Pairs)	References To Homologous GPCR	Per Cent Homology To Designated GPCR
hRUP8	AL131755	1,132bp	NPY2R	27%
hRUP9	AC0113375	1,260bp	GAL2R	22%
hRUP10	AC008743	1,014bp	CSaR	40%
hRUP11	AC013396	1,272bp	HM74	36%
hRUP12	AF000808	966bp	Mas1	34%
hRUP13	AC011780	1,356bp	Fish GPRX-ORVLA	43%
hRUP14	AL137118	1,041bp	CyLTLR	35%
hRUP15	AL016468	1,327bp	RET	30%
hRUP16	AL136106	1,068bp	GLR101	37%
hRUP17	AC023078	969bp	Mas1	37%
hRUP18	AC008547	1,305bp	Oxytocin	31%
hRUP19	AC026331	1,041bp	HM74	52%
hRUP20	AL161458	1,011bp	GPR34	23%
hRUP21	AC026756	1,014bp	P2Y1R	37%
hRUP22	AC027026	993bp	RUP17 Mas1	37%

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VECTOR in reference to cDNA shall mean a circular DNA, capable of incorporating at least one cDNA and capable of incorporation into a Host Cell.

The order of the following sections is set forth for presentational efficiency and is not intended, nor should be construed, as a limitation on the disclosure or the claims to follow.

A. Introduction

The traditional study of receptors has always proceeded from the a priori assumption (historically based) that the endogenous ligand must first be identified before discovery could proceed to find antagonists and other molecules that could affect the receptor. Even in cases where an antagonist might have been known first, the search immediately extended to looking for the endogenous ligand. This mode of thinking has persisted in receptor research even after the discovery of constitutively activated receptors. What has not been heretofore recognized is that it is the active state of the receptor that is most useful for discovering agonists, partial agonists, and inverse agonists of the receptor. For those diseases which result from an overly active receptor or an under-active receptor, what is desired in a therapeutic drug is a compound which acts to diminish the active state of a receptor or enhance the activity of the receptor, respectively, not necessarily a drug which is an antagonist to the endogenous ligand. This is because a compound that reduces or enhances the activity of the active receptor state need not bind at the same site as the endogenous ligand. Thus, as taught by a method of this invention, any search for therapeutic compounds should start by screening compounds against the ligand-independent active state.

B. Identification of Human GPCRs

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hRUP23	AC007104	1,092bp	Rat GPR26	31%
hRUP24	AL355388	1,125bp	SALPR	44%
hRUP25	AC026331	1,092bp	HM74	95%
hRUP26	AC023040	1,044bp	Rabbit 5HT1D	27%
hRUP27	AC027643	158,700	MCH	38%

Receptor homology is useful in terms of gaining an appreciation of a role of the receptors within the human body. As the patent document progresses, we will disclose techniques for mutating these receptors to establish non-endogenous, constitutively activated versions of these receptors.

The techniques disclosed herein have also been applied to other human, orphan GPCRs known to the art, as will be apparent as the patent document progresses.

C. Receptor Screening

Screening candidate compounds against a non-endogenous, constitutively activated version of the human GPCRs disclosed herein allows for the direct identification of candidate compounds which act at this cell surface receptor, without requiring use of the receptor's endogenous ligand. Using routine, and often commercially available techniques, one can determine areas within the body where the endogenous version of human GPCRs disclosed herein is expressed and/or over-expressed. It is also possible using these techniques to determine related disease/disorder states which are associated with the expression and/or over-expression of the receptor; such an approach is disclosed in this patent document.

With respect to creation of a mutation that may evidence constitutive activation of the human GPCR disclosed herein is based upon the distance from the proline residue at which is presumed to be located within TM6 of the GPCR; this algorithmic technique is disclosed in co-pending and commonly assigned patent document PCT Application

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Number PCT/US99/23938, published as WO 00/22129 on April 20, 2000, which, along with the other patent documents listed herein, is incorporated herein by reference. The algorithmic technique is not predicated upon traditional sequence "alignment" but rather a specified distance from the aforementioned TM6 proline residue (or, of course, endogenous constitutive substitution for such proline residue). By mutating the amino acid residue located 16 amino acid residues from this residue (presumably located in the IC3 region of the receptor) to, most preferably, a lysine residue, such activation may be obtained. Other amino acid residues may be useful in the mutation at this position to achieve this objective.

D. Disease/Disorder Identification and/or Selection

As will be set forth in greater detail below, most preferably inverse agonists and agonists to the non-endogenous, constitutively activated GPCR can be identified by the methodologies of this invention. Such inverse agonists and agonists are ideal candidates as lead compounds in drug discovery programs for treating diseases related to this receptor. Because of the ability to directly identify inverse agonists to the GPCR, thereby allowing for the development of pharmaceutical compositions, a search for diseases and disorders associated with the GPCR is relevant. For example, scanning both diseased and normal tissue samples for the presence of the GPCR now becomes more than an academic exercise or one which might be pursued along the path of identifying an endogenous ligand to the specific GPCR. Tissue scans can be conducted across a broad range of healthy and diseased tissues. Such tissue scans provide a preferred first step in associating a specific receptor with a disease and/or disorder.

Preferably, the DNA sequence of the human GPCR is used to make a probe for (a) dot-blot analysis against tissue-mRNA, and/or (b) RT-PCR identification of the expression of the receptor in tissue samples. The presence of a receptor in a tissue

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receptor site is preferred. For example, a compound identified by the "generic" assay may not bind to the receptor, but may instead merely "uncouple" the G protein from the intracellular domain.

a. Gs, Gz and Gi.

Gs stimulates the enzyme adenylyl cyclase. Gi (and Gz and Go), on the other hand, inhibit this enzyme. Adenylyl cyclase catalyzes the conversion of ATP to cAMP; thus, constitutively activated GPCRs that couple the Gs protein are associated with increased cellular levels of cAMP. On the other hand, constitutively activated GPCRs that couple Gi (or Gz, Go) protein are associated with decreased cellular levels of cAMP. See, generally, "Indirect Mechanisms of Synaptic Transmission," Chpt. 8, From Neuron To Brain (3rd Ed.) Nichols, J.G. et al eds. Sinauer Associates, Inc. (1992). Thus, assays that detect cAMP can be utilized to determine if a candidate compound is, e.g., an inverse agonist to the receptor (i.e., such a compound would decrease the levels of cAMP). A variety of approaches known in the art for measuring cAMP can be utilized; a most preferred approach relies upon the use of anti-cAMP antibodies in an ELISA-based format. Another type of assay that can be utilized is a whole cell second messenger reporter system assay. Promoters on genes drive the expression of the proteins that a particular gene encodes. Cyclic AMP drives gene expression by promoting the binding of a cAMP-responsive DNA binding protein or transcription factor (CREB) that then binds to the promoter at specific sites called cAMP response elements and drives the expression of the gene. Reporter systems can be constructed which have a promoter containing multiple cAMP response elements before the reporter gene, e.g., β -galactosidase or luciferase. Thus, a constitutively activated Gs-linked receptor causes the accumulation of cAMP that then activates the gene and expression of

source, or a diseased tissue, or the presence of the receptor at elevated concentrations in diseased tissue compared to a normal tissue, can be preferably utilized to identify a correlation with a treatment regimen, including but not limited to, a disease associated with that disease. Receptors can equally well be localized to regions of organs by this technique. Based on the known functions of the specific tissues to which the receptor is localized, the putative functional role of the receptor can be deduced.

E. Screening of Candidate Compounds

1. Generic GPCR screening assay techniques

When a G protein receptor becomes constitutively active, it binds to a G protein (e.g., Gq, Gs, Gi, Gz, Go) and stimulates the binding of GTP to the G protein. The G protein then acts as a GTPase and slowly hydrolyzes the GTP to GDP, whereby the receptor, under normal conditions, becomes deactivated. However, constitutively activated receptors continue to exchange GDP to GTP. A non-hydrolyzable analog of GTP, [³⁵S]GTPγS, can be used to monitor enhanced binding to membranes which express constitutively activated receptors. It is reported that [³⁵S]GTPγS can be used to monitor G protein coupling to membranes in the absence and presence of ligand. An example of this monitoring, among other examples well-known and available to those in the art, was reported by Traynor and Naborski in 1995. The preferred use of this assay system is for initial screening of candidate compounds because the system is generically applicable to all G protein-coupled receptors regardless of the particular G protein that interacts with the intracellular domain of the receptor.

2. Specific GPCR screening assay techniques

Once candidate compounds are identified using the "generic" G protein-coupled receptor assay (i.e., an assay to select compounds that are agonists, partial agonists, or inverse agonists), further screening to confirm that the compounds have interacted at the

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the reporter protein. The reporter protein such as β -galactosidase or luciferase can then be detected using standard biochemical assays (Chen et al. 1995).

b. Go and Gq.

Gq and Go are associated with activation of the enzyme phospholipase C, which in turn hydrolyzes the phospholipid PIP_2 , releasing two intracellular messengers: diacylglycerol (DAG) and inositol 1,4,5-trisphosphate (IP_3). Increased accumulation of IP_3 is associated with activation of Gq- and Go-associated receptors. See, generally, "Indirect Mechanisms of Synaptic Transmission," Chpt. 8, From Neuron To Brain (3rd Ed.) Nichols, J.G. et al eds. Sinauer Associates, Inc. (1992). Assays that detect IP_3 accumulation can be utilized to determine if a candidate compound is, e.g., an inverse agonist to a Gq- or Go-associated receptor (i.e., such a compound would decrease the levels of IP_3). Gq-associated receptors can also be examined using an AP1 reporter assay in that Gq-dependent phospholipase C causes activation of genes containing AP1 elements; thus, activated Gq-associated receptors will evidence an increase in the expression of such genes, whereby inverse agonists thereto will evidence a decrease in such expression, and agonists will evidence an increase in such expression. Commercially available assays for such detection are available.

3. GPCR Fusion Protein

The use of an endogenous, constitutively activate orphan GPCR or a non-endogenous, constitutively activated orphan GPCR, for use in screening of candidate compounds for the direct identification of inverse agonists, agonists and partial agonists provide an interesting screening challenge in that, by definition, the receptor is active even in the absence of an endogenous ligand bound thereto. Thus, in order to differentiate between, e.g., the non-endogenous receptor in the presence of a candidate compound and the non-endogenous receptor in the absence of that compound, with an

aim of such a differentiation to allow for an understanding as to whether such compound may be an inverse agonist, agonist, partial agonist or have no effect on such a receptor, it is preferred that an approach be utilized that can enhance such differentiation. A preferred approach is the use of a GPCR Fusion Protein.

Generally, once it is determined that a non-endogenous orphan GPCR has been constitutively activated using the assay techniques set forth above (as well as others), it is possible to determine the predominant G protein that couples with the endogenous GPCR. Coupling of the G protein to the GPCR provides a signaling pathway that can be assessed. Because it is most preferred that screening take place by use of a mammalian expression system, such a system will be expected to have endogenous G protein therein. Thus, by definition, in such a system, the non-endogenous, constitutively activated orphan GPCR will continuously signal. In this regard, it is preferred that this signal be enhanced such that in the presence of, e.g., an inverse agonist to the receptor, it is more likely that it will be able to more readily differentiate, particularly in the context of screening, between the receptor when it is contacted with the inverse agonist.

The GPCR Fusion Protein is intended to enhance the efficacy of G protein coupling with the non-endogenous GPCR. The GPCR Fusion Protein is preferred for screening with a non-endogenous, constitutively activated GPCR because such an approach increases the signal that is most preferably utilized in such screening techniques. This is important in facilitating a significant "signal to noise" ratio; such a significant ratio is import preferred for the screening of candidate compounds as disclosed herein.

The construction of a construct useful for expression of a GPCR Fusion Protein is within the purview of those having ordinary skill in the art. Commercially available expression vectors and systems offer a variety of approaches that can fit the particular

the endogenous GPCR to couple with, e.g., Gs rather than the "natural" Gi protein, such that a cyclase-based assay can be established. Thus, for Gi, Gz and Go coupled receptors, we prefer that when a GPCR Fusion Protein is used and the assay is based upon detection of adenylyl cyclase activity, that the fusion construct be established with Gs (or an equivalent G protein that stimulates the formation of the enzyme adenylyl cyclase).

Equally effective is a G Protein Fusion construct that utilizes a Gq Protein fused with a Gs, Gi, Gz or Go Protein. A most preferred fusion construct can be accomplished with a Gq Protein wherein the first six (6) amino acids of the G-protein α -subunit ("G α q") is deleted and the last five (5) amino acids at the C-terminal end of G α q is replaced with the corresponding amino acids of the G α of the G protein of interest. For example, a fusion construct can have a Gq (6 amino acid deletion) fused with a Gi Protein, resulting in a "Gq/Gi Fusion Construct". We believe that this fusion construct will force the endogenous Gi coupled receptor to couple to its non-endogenous G protein, Gq, such that the second messenger, for example, inositol triphosphate or diacylglycerol, can be measured in lieu of cAMP production.

4. Co-transfection of a Target Gi Coupled GPCR with a Signal-Enhancer Gs Coupled GPCR (cAMP Based Assays)

A Gi coupled receptor is known to inhibit adenylyl cyclase, and, therefore, decrease the level of cAMP production, which can make assessment of cAMP levels challenging. An effective technique in measuring the decrease in production of cAMP as an indication of constitutive activation of a receptor that predominantly couples Gi upon activation can be accomplished by co-transfecting a signal enhancer, e.g., a non-endogenous, constitutively activated receptor that predominantly couples with Gs upon activation (e.g., TSHR-A6231, disclosed below), with the Gi linked GPCR. As is

needs of an investigator. The criteria of importance for such a GPCR Fusion Protein construct is that the endogenous GPCR sequence and the G protein sequence both be in-frame (preferably, the sequence for the endogenous GPCR is upstream of the G protein sequence) and that the "stop" codon of the GPCR must be deleted or replaced such that upon expression of the GPCR, the G protein can also be expressed. The GPCR can be linked directly to the G protein, or there can be spacer residues between the two (preferably, no more than about 12, although this number can be readily ascertained by one of ordinary skill in the art). We have a preference (based upon convenience) of use of a spacer in that some restriction sites that are not used will, effectively, upon expression, become a spacer. Most preferably, the G protein that couples to the non-endogenous GPCR will have been identified prior to the creation of the GPCR Fusion Protein construct. Because there are only a few G proteins that have been identified, it is preferred that a construct comprising the sequence of the G protein (i.e., a universal G protein construct) be available for insertion of an endogenous GPCR sequence therein; this provides for efficiency in the context of large-scale screening of a variety of different endogenous GPCRs having different sequences.

As noted above, constitutively activated GPCRs that couple to Gi, Gz and Go are expected to inhibit the formation of cAMP making assays based upon these types of GPCRs challenging (i.e., the cAMP signal decreases upon activation thus making the direct identification of, e.g., inverse agonists (which would further decrease this signal), interesting. As will be disclosed herein, we have ascertained that for these types of receptors, it is possible to create a GPCR Fusion Protein that is not based upon the endogenous GPCR's endogenous G protein, in an effort to establish a viable cyclase-based assay. Thus, for example, an endogenous Gi coupled receptor can be fused to a Gs protein - we believe that such a fusion construct, upon expression, "drives" or "forces"

apparent, constitutive activation of a Gs coupled receptor can be determined based upon an increase in production of cAMP. Constitutive activation of a Gi coupled receptor leads to a decrease in production cAMP. Thus, the co-transfection approach is intended to advantageously exploit these "opposite" effects. For example, co-transfection of a non-endogenous, constitutively activated Gs coupled receptor (the "signal enhancer") with the endogenous Gi coupled receptor (the "target receptor") provides a baseline cAMP signal (i.e., although the Gi coupled receptor will decrease cAMP levels, this "decrease" will be relative to the substantial increase in cAMP levels established by constitutively activated Gs coupled signal enhancer). By then co-transfecting the signal enhancer with a constitutively activated version of the target receptor, cAMP would be expected to further decrease (relative to base line) due to the increased functional activity of the Gi target (i.e., which decreases cAMP).

Screening of candidate compounds using a cAMP based assay can then be accomplished, with two provisos: first, relative to the Gi coupled target receptor, "opposite" effects will result, i.e., an inverse agonist of the Gi coupled target receptor will increase the measured cAMP signal, while an agonist of the Gi coupled target receptor will decrease this signal; second, as would be apparent, candidate compounds that are directly identified using this approach should be assessed independently to ensure that these do not target the signal enhancing receptor (this can be done prior to or after screening against the co-transfected receptors).

F. Medicinal Chemistry

Generally, but not always, direct identification of candidate compounds is preferably conducted in conjunction with compounds generated via combinatorial chemistry techniques, whereby thousands of compounds are randomly prepared for such analysis. Generally, the results of such screening will be compounds having

unique core structures; thereafter, these compounds are preferably subjected to additional chemical modification around a preferred core structure(s) to further enhance the medicinal properties thereof. Such techniques are known to those in the art and will not be addressed in detail in this patent document.

G. Pharmaceutical compositions

Candidate compounds selected for further development can be formulated into pharmaceutical compositions using techniques well known to those in the art. Suitable pharmaceutically-acceptable carriers are available to those in the art; for example, see Remington's Pharmaceutical Sciences, 16th Edition, 1980, Mack Publishing Co., (Oslo et al., eds.).

H. Other Utility

Although a preferred use of the non-endogenous versions the human GPCRs disclosed herein may be for the direct identification of candidate compounds as inverse agonists, agonists or partial agonists (preferably for use as pharmaceutical agents), these versions of human GPCRs can also be utilized in research settings. For example, *in vitro* and *in vivo* systems incorporating GPCRs can be utilized to further elucidate and understand the roles these receptors play in the human condition, both normal and diseased, as well as understanding the role of constitutive activation as it applies to understanding the signaling cascade. The value in non-endogenous human GPCRs is that their utility as a research tool is enhanced in that, because of their unique features, non-endogenous human GPCRs can be used to understand the role of these receptors in the human body before the endogenous ligand therefore is identified. Other uses of the disclosed receptors will become apparent to those in the art based upon, *inter alia*, a review of this patent document.

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TABLE C

Disclosed Human Orphan GPCRs	Accession Number Identified	Complete DNA Sequence (Base Pairs)	Open Reading Frame (Base Pairs)	Nucleic Acid SEQ.ID. NO.	Amino Acid SEQ.ID. NO.
hRUP8	AL121755	147,566bp	1,152bp	1	2
hRUP9	AC0113375	143,181bp	1,260bp	3	4
hRUP10	AC008745	94,194bp	1,014bp	5	6
hRUP11	AC013396	135,048bp	1,272bp	7	8
hRUP12	AF000808	177,764bp	966bp	9	10
hRUP13	AC011780	167,819bp	1,356bp	11	12
hRUP14	AL137118	168,297bp	1,041bp	13	14
hRUP15	AL016468	138,828bp	1,527bp	15	16
hRUP16	AL136106	208,042bp	1,068bp	17	18
hRUP17	AC023078	161,735bp	969bp	19	20
hRUP18	AC008547	117,304bp	1,305bp	21	22
hRUP19	AC026331	145,183bp	1,041bp	23	24
hRUP20	AL161458	163,511bp	1,011bp	25	26
hRUP21	AC026756	156,334bp	1,014bp	27	28
hRUP22	AC027026	151,811bp	993bp	29	30
hRUP23	AC007104	200,000bp	1,092bp	31	32
hRUP24	AL355388	190,338bp	1,125bp	33	34
hRUP25	AC026331	145,183bp	1,092bp	35	36
hRUP26	AC023040	178,508bp	1,044bp	37	38
hRUP27	AC027643	158,700bp	1,020bp	39	40

2. Full Length Cloning

a. hRUP8 (Seq. Id. Nos. 1 & 2)

The disclosed human RUP8 was identified based upon the use of EST database (*dbEST*) information. While searching the *dbEST*, a cDNA clone with accession number

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EXAMPLES

The following examples are presented for purposes of elucidation, and not limitation, of the present invention. While specific nucleic acid and amino acid sequences are disclosed herein, those of ordinary skill in the art are credited with the ability to make minor modifications to these sequences while achieving the same or substantially similar results reported below. The traditional approach to application or understanding of sequence cassettes from one sequence to another (e.g. from rat receptor to human receptor or from human receptor A to human receptor B) is generally predicated upon sequence alignment techniques whereby the sequences are aligned in an effort to determine areas of commonality. The mutational approach disclosed herein does not rely upon this approach but is instead based upon an algorithmic approach and a positional distance from a conserved proline residue located within the TM6 region of human GPCRs. Once this approach is secured, those in the art are credited with the ability to make minor modifications thereto to achieve substantially the same results (*i.e.*, constitutive activation) disclosed herein. Such modified approaches are considered within the purview of this disclosure.

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Example 1 ENDOGENOUS HUMAN GPCRS

1. Identification of Human GPCRs

The disclosed endogenous human GPCRs were identified based upon a review of the GenBank™ database information. While searching the database, the following cDNA clones were identified as evidenced below (Table C).

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AL121755 was identified to encode a novel GPCR. The following PCR primers were used for RT-PCR with human testis Marathon-Ready cDNA (Clontech) as templates:

5'-CTTGCAGACATCAACATGGCAGCC-3' (SEQ.ID.NO.:41; sense) and

5'-GTGATGCTCTGAGTACTGGACTGG-3' (SEQ.ID.NO.: 42; antisense).

PCR was performed using Advantage cDNA polymerase (Clontech; manufacturing instructions will be followed) in 50ul reaction by the following cycles: 94°C for 30 sec; 94°C for 10 sec; 65°C for 20 sec, 72°C for 1.5 min, and 72°C for 7 min. Cycles 2 through 4 were repeated 35 times.

A 1.2kb PCR fragment was isolated and cloned into the pCRII-TOPO vector (Invitrogen) and sequenced using the ABI Big Dye Terminator kit (P.E. Biosystem). See, SEQ.ID.NO.:1. The putative amino acid sequence for RUP8 is set forth in SEQ.ID.NO.:2.

b. hRUP9 (Seq. Id. Nos. 3 & 4)

The disclosed human RUP9 was identified based upon the use of GeneBank database information. While searching the database, a cDNA clone with Accession Number AC011375 was identified as a human genomic sequence from chromosome 5. The full length RUP9 was cloned by PCR using primers:

5'-GAAGCTGTGAAGAGTGATGC-3' (SEQ.ID.NO.:43; sense),

5'-GTCAGCAATATTGATAAGCAGCAG-3' (SEQ.ID.NO.:44; antisense)

and human genomic DNA (Promega) as a template. Taq Plus Precision polymerase (Stratagene) was used for the amplification in a 100ul reaction with 5% DMSO by the following cycle with step 2 to step 4 repeated 35 times: 94°C for 1 minute; 94°C for 30 seconds; 56°C for 30 seconds; 72°C for 2 minutes; 72°C for 5 minutes.

A 1.3 Kb PCR fragment was isolated and cloned into the pCRII-TOPO vector (Invitrogen) from 1% agarose gel and completely sequenced using the ABI Big Dye

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Terminator kit (P.E. Biosystem). See, SEQ.ID.NO.:3. The putative amino acid sequence for RUP8 is set forth in SEQ.ID.NO.:4. The sequence of RUP9 clones isolated from human genomic DNA matched with the sequence obtained from data base.

c. hRUP10 (Seq. Id. Nos. 5 & 6)

The disclosed human RUP10 was identified based upon the use of GenBank database information. While searching the database, a cDNA clone with accession number AC008754 was identified as a human genomic sequence from chromosome 19. The full length RUP10 was cloned by RT-PCR using primers:

5'-CCATGGGGAACGATTCTCTCAGCTACG-3' (SEQ.ID.NO.:45; sense) and

5'-GCTATGCCTGAAGCCAGTCTTGTG-3' (SEQ.ID.NO.:46; antisense)

and human leukocyte Marathon-Ready cDNA (Clontech) as a template. Advantage cDNA polymerase (Clontech) was used for the amplification in a 50µl reaction by the following cycle with step 2 to step 4 repeated 35 times: 94°C for 30 seconds; 94°C for 10 seconds; 62°C for 20 seconds; 72°C for 1.5 minutes; 72°C for 7 minutes. A 1.0 Kb PCR fragment was isolated and cloned into the pCRII-TOPO vector (Invitrogen) and completely sequenced using the ABI Big Dye Terminator kit (P.E. Biosystem). The nucleic acid sequence of the novel human receptor RUP10 is set forth in SEQ.ID.NO.:5 and the putative amino acid sequence thereof is set forth in SEQ.ID.NO.:6.

d. hRUP11 (Seq. Id. Nos. 7 & 8)

The disclosed human RUP11 was identified based upon the use of GenBank database information. While searching the database, a cDNA clone with accession number AC013396 was identified as a human genomic sequence from chromosome 2.

(P.E. Biosystem) (see, SEQ.ID.NO.:9 for nucleic acid sequence and SEQ.ID.NO.:10 for deduced amino acid sequence).

f. hRUP13 (Seq. Id. Nos. 11 & 12)

The disclosed human RUP13 was identified based upon the use of GenBank database. While searching the database, a cDNA clone with accession number AC011780 was identified to encode a new GPCR, having significant homology with GPCR fish GPRX-ORYLA. The full length RUP13 was cloned by PCR using primers:

5'-GCCTGTGACAGGAGGTACCCCTGG-3' (SEQ.ID.NO.:51; sense)

5'-CATATCCCTCCGAGTGTCCAGGGGC-3' (SEQ.ID.NO.:52; antisense)

and human genomic DNA (Clontech) as template. TaqPlus Precision DNA polymerase (Stratagene) was used for the amplification by the following cycle with step 2 to step 4 repeated 35 times: 94°C for 3 min; 94°C for 20 sec; 65°C for 20sec; 72°C for 2 min and 72°C for 7 min. A 1.35kb PCR fragment was isolated and cloned into the pCRII-TOPO vector (Invitrogen) and completely sequenced using the ABI Big Dye Terminator kit (P.E. Biosystem) (see, SEQ.ID.NO.:11 for nucleic acid sequence and SEQ.ID.NO.:12 for deduced amino acid sequence).

g. hRUP14 (Seq. Id. Nos. 13 & 14)

The disclosed human RUP14 was identified based upon the use of GenBank database information. While searching the database, a cDNA clone with Accession Number AL137118 was identified as a human genomic sequence from chromosome 13. The full length RUP14 was cloned by PCR using primers:

5'-GCATGGAGAGAAAAATTATGTCTTCAACC-3' (SEQ.ID.NO.:53; sense)

5'-CAAGAACAGGTCTCATCTAAGACTCC-3' (SEQ.ID.NO.:54; antisense)

and human genomic DNA (Promega) as a template. Taq Plus Precision polymerase (Stratagene) and 5% DMSO were used for the amplification by the following cycle

The full length RUP11 was cloned by PCR using primers:

5'-CCAGGATGTTGTGTCACCGTGGTGGC-3' (SEQ.ID.NO.:47; sense),

5'-CACAGCGCTGCAGCCCTGCAGCTGGC-3' (SEQ.ID.NO.:48; antisense)

and human genomic DNA (Clontech) as a template. TaqPlus Precision DNA polymerase (Stratagene) was used for the amplification in a 50µl reaction by the following cycle with step 2 to step 4 repeated 35 times: 94°C for 3 minutes; 94°C for 20 seconds; 67°C for 20 seconds; 72°C for 1.5 minutes; 72°C for 7 minutes. A 1.3 Kb PCR fragment was isolated and cloned into the pCRII-TOPO vector (Invitrogen) and completely sequenced using the ABI Big Dye Terminator kit (P.E. Biosystem). The nucleic acid sequence of the novel human receptor RUP11 is set forth in SEQ.ID.NO.:7 and the putative amino acid sequence thereof is set forth in SEQ.ID.NO.:8.

e. hRUP12 (Seq. Id. Nos. 9 & 10)

The disclosed human RUP12 was identified based upon the use of GenBank database. While searching the database, a cDNA clone with accession number AP000808 was identified to encode a new GPCR, having significant homology with rat RTA and human mas1 oncogene GPCRs. The full length RUP12 was cloned by PCR using primers:

5'-CTTCTCTCTGTAGGGATGAACAGAC-3' (SEQ.ID.NO.:49; sense)

5'-CTCGCACAGTGGGAAGCACTGTGG-3' (SEQ.ID.NO.:50; antisense)

and human genomic DNA (Clontech) as template. TaqPlus Precision DNA polymerase (Stratagene) was used for the amplification by the following cycle with step 2 to step 4 repeated 35 times: 94°C for 3 min; 94°C for 20 sec; 65°C for 20sec; 72°C for 2 min and 72°C for 7 min. A 1.0kb PCR fragment was isolated and cloned into the pCRII-TOPO vector (Invitrogen) and completely sequenced using the ABI Big Dye Terminator kit

with step 2 and step 3 repeated 35 times: 94°C for 3 minute; 94°C for 20 seconds; 58°C for 2 minutes; 72°C for 10 minutes.

A 1.1-Kb PCR fragment was isolated and cloned into the pCRII-TOPO vector (Invitrogen) and completely sequenced using the ABI Big Dye Terminator kit (P.E. Biosystem) (see, SEQ.ID.NO.:13 for nucleic acid sequence and SEQ.ID.NO.:14 for deduced amino acid sequence). The sequence of RUP14 clones isolated from human genomic DNA matched with the sequence obtained from database.

h. hRUP15 (Seq. Id. Nos. 15 & 16)

The disclosed human RUP15 was identified based upon the use of GenBank database information. While searching the database, a cDNA clone with Accession Number AC016468 was identified as a human genomic sequence. The full length RUP15 was cloned by PCR using primers:

5'-GCTGTGTCATGACGTCCACCTGCAC-3' (SEQ.ID.NO.:55; sense)

5'-GGACAGTTCAGGTTTCCTTAGAAC-3' (SEQ.ID.NO.:56; antisense)

and human genomic DNA (Promega) as a template. Taq Plus Precision polymerase (Stratagene) was used for the amplification by the following cycle with step 2 to 4 repeated 35 times: 94°C for 3 minute; 94°C for 20 seconds; 65°C for 20 seconds; 72°C for 2 minutes and 72°C for 7 minutes.

A 1.5 Kb PCR fragment was isolated and cloned into the pCRII-TOPO vector (Invitrogen) and completely sequenced using the ABI Big Dye Terminator kit (P.E. Biosystem). See, SEQ.ID.NO.:15 for nucleic acid sequence and SEQ.ID.NO.:16 for deduced amino acid sequence. The sequence of RUP15 clones isolated from human genomic DNA matched with the sequence obtained from database.

i. hRUP16 (Seq. Id. Nos. 17 & 18)

The disclosed human RUP16 was identified based upon the use of GeneBank database information. While searching the database, a cDNA clone with Accession Number AL136106 was identified as a human genomic sequence from chromosome 13. The full length RUP16 was cloned by PCR using primers:

- 5' -CTTTGATACTGCTCTATGCTC-3' (SEQ.ID.NO.:57; sense, 5' of initiation codon),
 5' -GTAGTCCACTGAAAGTCCAGTGATCC-3' (SEQ.ID.NO.:58; antisense, 3' of stop codon)
 and human skeletal muscle Marathon-Ready cDNA (Clontech) as template. Advantage cDNA polymerase (Clontech) was used for the amplification in a 50ul reaction by the following cycle with step 2 to 4 repeated 35 times: 94°C for 30 seconds; 94°C for 5
 10 seconds; 69°C for 15 seconds; 72°C for 1 minute and 72°C for 5 minutes.

A 1.1 Kb PCR fragment was isolated and cloned into the pCRII-TOPO vector (Invitrogen) and completely sequenced using the T7 sequenase kit (Amsham). See, SEQ.ID.NO.:17 for nucleic acid sequence and SEQ.ID.NO.:18 for deduced amino acid sequence. The sequence of RUP16 clones matched with four unordered segments of
 15 AL136106, indicating that the RUP16 cDNA is composed of 4 exons.

j. hRUP17 (Seq. Id. Nos. 19 & 20)

The disclosed human RUP17 was identified based upon the use of GeneBank database information. While searching the database, a cDNA clone with Accession Number AC023078 was identified as a human genomic sequence from chromosome

- 20 11. The full length RUP17 was cloned by PCR using primers:
 5'-TTTCTGAGCATGGATCCAACTCTC-3' (SEQ.ID.NO.:59; sense, containing initiation codon)
 5'-CTGTCTGACAGGGCAGAGGCTCTTC-3' (SEQ.ID.NO.:60; antisense, 3' of stop codon)
 and human genomic DNA (Promega) as template. Advantage cDNA polymerase mix
 25 (Clontech) was used for the amplification in a 100ul reaction with 5% DMSO by the

The disclosed human RUP19 was identified based upon the use of GeneBank database information. While searching the database, a cDNA clone with Accession Number AC026331 was identified as a human genomic sequence from chromosome 12. The full length RUP19 was cloned by PCR using primers:

- 5' -CTGCACCCGGACACTTGCTCTG-3' (SEQ.ID.NO.:63; sense, 5' of initiation codon),
 5' -GTCTGCTTGTTCAGTGCCACTCAAC-3' (SEQ.ID.NO.:64; antisense, containing the stop codon)

and human genomic DNA (Promega) as template. TaqPlus Precision DNA polymerase (Stratagene) was used for the amplification with 5% DMSO by the following cycle with step 2 to 4 repeated 35 times: 94°C for 1 min; 94°C for 15 sec;
 10 70°C for 20 sec; 72°C for 1 min and 30 sec; and 72°C for 5 min.

A 1.1kp PCR fragment was isolated from 1% agarose gel and cloned into the pCRII-TOPO vector (Invitrogen) and completely sequenced using the ABI Big Dye Terminator Kit (P.E. Biosystem). See, SEQ.ID.NO.:23 for nucleic acid sequence and
 15 SEQ.ID.NO.:24 for deduced amino acid sequence.

m. hRUP20 (Seq. Id. Nos. 25 & 26)

The disclosed human RUP20 was identified based upon the use of GeneBank database information. While searching the database, a cDNA clone with Accession Number AL161458 was identified as a human genomic sequence from chromosome

- 20 1. The full length RUP20 was cloned by PCR using primers:
 5'-TATCTGCAATTCTATTCTAGCTCTG-3' (SEQ.ID.NO.:65; sense, 5' of initiation codon),
 5'-TGTCCTAATAAAGTCACATGAATGC-3' (SEQ.ID.NO.:66; antisense, 3' of stop codon)
 and human genomic DNA (Promega) as template. Advantage cDNA polymerase mix
 (Clontech) was used for the amplification with 5% DMSO by the following cycle with

following cycle with step 2 to 4 repeated 30 times: 94°C for 1 min; 94°C for 15 sec;
 67°C for 20 sec; 72°C for 1 min and 30 sec; and 72°C for 5 min.

A 970bp PCR fragment was isolated from 1% agarose gel and cloned into the pCRII-TOPO vector (Invitrogen) and completely sequenced using the ABI Big Dye Terminator Kit (P.E. Biosystem). See, SEQ.ID.NO.:19 for nucleic acid sequence and
 5 SEQ.ID.NO.:20 for deduced amino acid sequence.

k. hRUP18 (Seq. Id. Nos. 21 & 22)

The disclosed human RUP18 was identified based upon the use of GeneBank database information. While searching the database, a cDNA clone with Accession Number AC008547 was identified as a human genomic sequence from chromosome
 10 5. The full length RUP18 was cloned by PCR using primers:

- 5'-GGAACCTGATATAGACCCAGCGTGGCTCC-3' (SEQ.ID.NO.:61; sense, 5' of the initiation codon),
 5'-GGAGGTTGCGCCTTAGCGACAGATGACC-3' (SEQ.ID.NO.:62; antisense, 3' of stop codon)

and human genomic DNA (Promega) as template. TaqPlus precision DNA polymerase (Stratagene) was used for the amplification in a 100ul reaction with 5% DMSO by the following cycle with step 2 to 4 repeated 35 times: 95°C for 5 min;
 95°C for 30 sec; 65°C for 30 sec; 72°C for 2 min; and 72°C for 5 min.

A 1.3kb PCR fragment was isolated from 1% agarose gel and cloned into the pCRII-TOPO vector (Invitrogen) and completely sequenced using the ABI Big Dye Terminator Kit (P.E. Biosystem). See, SEQ.ID.NO.:21 for nucleic acid sequence and
 20 SEQ.ID.NO.:22 for deduced amino acid sequence.

l. hRUP19 (Seq. Id. Nos. 23 & 24)

step 2 to 4 repeated 35 times: 94°C for 1 min; 94°C for 15 sec; 60°C for 20 sec; 72°C
 for 1 min and 30 sec; and 72°C for 5 min.

A 1.0 kp PCR fragment was isolated from 1% agarose gel and cloned into the pCRII-TOPO vector (Invitrogen) and completely sequenced using the ABI Big Dye Terminator Kit (P.E. Biosystem). See, SEQ.ID.NO.:25 for nucleic acid sequence and
 5 SEQ.ID.NO.:26 for deduced amino acid sequence.

n. hRUP21 (Seq. Id. Nos. 27 & 28)

The disclosed human RUP21 was identified based upon the use of GeneBank database information. While searching the database, a cDNA clone with Accession Number AC026756 was identified as a human genomic sequence from chromosome
 10 13. The full length RUP21 was cloned by PCR using primers:

- 5'-GGAGACAACCATGAATGAGGCAC-3' (SEQ.ID.NO.:67; sense)
 5'-TATTTCAAGGGTTGTTGAGTAAC-3' (SEQ.ID.NO.:68; antisense)

and human genomic DNA (Promega) as template. Taq Plus Precision polymerase (Stratagene) was used for the amplification in a 100ul reaction with 5% DMSO by the following cycle with step 2 to 4 repeated 30 times: 94°C for 1 min; 94°C for 15 sec;
 15 55°C for 20 sec; 72°C for 1 min and 30 sec; and 72°C for 5 min.

A 1,014 bp PCR fragment was isolated from 1% agarose gel and cloned into the pCRII-TOPO vector (Invitrogen) and completely sequenced using the ABI Big Dye Terminator Kit (P.E. Biosystem). See, SEQ.ID.NO.:27 for nucleic acid sequence and
 20 SEQ.ID.NO.:28 for deduced amino acid sequence.

o. hRUP22 (Seq. Id. Nos. 29 & 30)

The disclosed human RUP22 was identified based upon the use of GeneBank database information. While searching the database, a cDNA clone with Accession

Number AC027026 was identified as a human genomic sequence from chromosome

11. The full length RUP22 was cloned by PCR using primers:

5'-GGCAACAGTGGAGGTTTCTGAGCATG-3' (SEQ.ID.NO.:69; sense, containing initiation codon)

5'-CTGATGGAAGTAGAGGCTGTCCATCTC-3' (SEQ.ID.NO.:70; antisense, 3' of stop codon)

and human genomic DNA (Promega) as template. TaqPlus Precision DNA polymerase (Stratagene) was used for the amplification in a 100ul reaction with 5% DMSO by the following cycle with step 2 to 4 repeated 30 times: 94°C, 1 minutes 94°C, 15 seconds 55°C, 20 seconds 72°C, 1.5 minute 72°C, 5 minutes.

A 970bp PCR fragment was isolated from 1% agarose gel and cloned into the pCRII-TOPO vector (Invitrogen) and completely sequenced using the ABI Big Dye Terminator Kit (P.E. Biosystem). See, SEQ.ID.NO.:29 for nucleic acid sequence and SEQ.ID.NO.:30 for deduced amino acid sequence.

p. hRUP23 (Seq. Id. Nos. 31 & 32)

The disclosed human RUP23 was identified based upon the use of GeneBank database information. While searching the database, a cDNA clone with Accession Number AC007104 was identified as a human genomic sequence from chromosome 4. The full length RUP23 was cloned by PCR using primers:

5'-OCTGGCGAGCGCTAGCGCCATG-3' (SEQ.ID.NO.:71; sense, ATG as the initiation codon),

5'-ATGAGCCCTGCGAGGCCCTCAGT-3' (SEQ.ID.NO.:72; antisense, TCA as the stop codon)

and human placenta Marathon-Ready cDNA (Clontech) as template. Advantage cDNA polymerase (Clontech) was used for the amplification in a 50ul reaction by the following

Number AC026331 was identified as a human genomic sequence from chromosome

12. The full length RUP25 was cloned by PCR using primers:

5'-GCTGGAGCATTCACTAGGCGAG-3' (SEQ.ID.NO.:75; sense, 5' of initiation codon),

5'-AGATCCTGGTTCTTGGTGACAATG-3' (SEQ.ID.NO.:76; antisense, 3' of stop codon)

and human genomic DNA (Promega) as template. Advantage cDNA polymerase mix (Clontech) was used for the amplification with 5% DMSO by the following cycle with step 2 to 4 repeated 35 times: 94°C for 1 minute; 94°C for 15 seconds; 56°C for 20 seconds 72°C for 1 minute 30 seconds and 72°C for 5 minutes.

A 1.2kb PCR fragment was isolated from 1% agarose gel and cloned into the pCRII-TOPO vector (Invitrogen) and completely sequenced using the ABI Big Dye Terminator Kit (P.E. Biosystem). See, SEQ.ID.NO.:35 for nucleic acid sequence and SEQ.ID.NO.:36 for deduced amino acid sequence.

a. hRUP26 (Seq. Id. Nos. 37 & 38)

The disclosed human RUP26 was identified based upon the use of GeneBank database information. While searching the database, a cDNA clone with Accession Number AC023040 was identified as a human genomic sequence from chromosome

2. The full length RUP26 was cloned by RT-PCR using RUP26 specific primers:

5'-AGCCATCCTGCGCAAGCATGG-3' (SEQ.ID.NO.:77; sense, containing initiation codon)

5'-OCAGACTGTGACTCAAGAACTTAGG-3' (SEQ.ID.NO.:78; antisense, containing stop codon)

and human pancreas Marathon-Ready cDNA (Clontech) as template. Advantage cDNA polymerase mix (Clontech) was used for the amplification in a 100ul reaction with 5% DMSO by the following cycle with step 2 to 4 repeated 35 times: 94°C for 5 minute; 95°C for 30 seconds; 65°C for 30 seconds 72°C for 2 minute and 72°C for 5 minutes.

cycle with step 2 to 4 repeated 35 times: 95°C for 30 sec; 95°C for 15 sec; 66°C for 20 sec; 72°C for 1 min and 20 sec; and 72°C for 5 min.

A 1.0 kb PCR fragment was isolated and cloned into the pCRII-TOPO vector (Invitrogen) and completely sequenced using the ABI Big Dye Terminator Kit (P.E. Biosystem). See, SEQ.ID.NO.:31 for nucleic acid sequence and SEQ.ID.NO.:32 for deduced amino acid sequence.

q. hRUP24 (Seq. Id. Nos. 33 & 34)

The disclosed human RUP25 was identified based upon the use of GeneBank database information. While searching the database, a cDNA clone with Accession Number AC026331 was identified as a human genomic sequence from chromosome 12. The full length RUP25 was cloned by PCR using primers:

5'-GCTGGAGCATTCACTAGGCGAG-3' (SEQ.ID.NO.:73; sense, 5' of initiation codon),

5'-AGATCCTGGTTCTTGGTGACAATG-3' (SEQ.ID.NO.:74; antisense, 3' of stop codon)

and human genomic DNA (Promega) as template. Advantage cDNA polymerase mix (Clontech) was used for the amplification with 5% DMSO by the following cycle with step 2 to 4 repeated 35 times: 94°C for 1 minute; 94°C for 15 seconds; 56°C for 20 seconds 72°C for 1 minute 30 seconds and 72°C for 5 minutes.

A 1.2kb PCR fragment was isolated from 1% agarose gel and cloned into the pCRII-TOPO vector (Invitrogen) and completely sequenced using the ABI Big Dye Terminator Kit (P.E. Biosystem). See, SEQ.ID.NO.:33 for nucleic acid sequence and SEQ.ID.NO.:34 for deduced amino acid sequence.

r. hRUP25 (Seq. Id. Nos. 35 & 36)

The disclosed human RUP25 was identified based upon the use of GeneBank database information. While searching the database, a cDNA clone with Accession

A 1.1kb PCR fragment was isolated from 1% agarose gel and cloned into the pCRII-TOPO vector (Invitrogen) and completely sequenced using the ABI Big Dye Terminator Kit (P.E. Biosystem). See, SEQ.ID.NO.:37 for nucleic acid sequence and SEQ.ID.NO.:38 for deduced amino acid sequence.

t. hRUP27 (Seq. Id. Nos. 39 & 40)

The disclosed human RUP27 was identified based upon the use of GeneBank database information. While searching the database, a cDNA clone with Accession Number AC027643 was identified as a human genomic sequence from chromosome 12. The full length RUP27 was cloned by PCR using RUP27 specific primers:

5'-AGTCCACGAACAATGAATCCATTTCATG-3' (SEQ.ID.NO.:79; sense, containing initiation codon),

5'-ATCATGTCTAGACTCATGGTGATCC-3' (SEQ.ID.NO.:80; antisense, 3' of stop codon)

and the human adult brain Marathon-Ready cDNA (Clontech) as template. Advantage cDNA polymerase mix (Clontech) was used for the amplification in a 50ul reaction with 5% DMSO by the following cycle with step 2 to 4 repeated 35 times: 94°C for 1 minute; 94°C for 10 seconds; 58°C for 20 seconds 72°C for 1 minute 30 seconds and 72°C for 5 minutes.

A 1.1kb PCR fragment was isolated from 1% agarose gel and cloned into the pCRII-TOPO vector (Invitrogen) and completely sequenced using the ABI Big Dye Terminator Kit (P.E. Biosystem). See, SEQ.ID.NO.:35 for nucleic acid sequence and SEQ.ID.NO.:36 for deduced amino acid sequence. The sequence of RUP27 cDNA clone isolated from human brain was determined to match with five unordered segments of AC027643, indicating that the RUP27 cDNA is composed of 5 exons.

Example 2 PREPARATION OF NON-ENDOGENOUS, CONSTITUTIVELY ACTIVATED GPCRS

Those skilled in the art are credited with the ability to select techniques for mutation of a nucleic acid sequence. Presented below are approaches utilized to create non-endogenous versions of several of the human GPCRs disclosed above. The mutations disclosed below are based upon an algorithmic approach whereby the 16th amino acid (located in the IC3 region of the GPCR) from a conserved proline (or an endogenous, conservative substitution therefore) residue (located in the TM6 region of the GPCR, near the TM6/IC3 interface) is mutated, preferably to an alanine, histidine, arginine or lysine amino acid residue, most preferably to a lysine amino acid residue.

1. Transformer Site-Directed™ Mutagenesis

Preparation of non-endogenous human GPCRs may be accomplished on human GPCRs using Transformer Site-Directed™ Mutagenesis Kit (Clontech) according to the manufacturer instructions. Two mutagenesis primers are utilized, most preferably a lysine mutagenesis oligonucleotide that creates the lysine mutation, and a selection marker oligonucleotide. For convenience, the codon mutation to be incorporated into the human GPCR is also noted, in standard form (Table D):

TABLE D

Receptor Identifier	Codon Mutation
hRUP8	V274K
hRUP9	T249K
hRUP10	R232K
hRUP11	M294K
hRUP12	F220K
hRUP16	A338K

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hRUP13	A398K	CCAGTGCAGAAAGCTAAG AAAGTGATCTTC (89)	GAAGATGACCTTCTTA GCTTGCACTGG (90)	98° for 2' 98° for 30" 55°C for 30" 72° for 11' 40" 72° for 5'
hRUP23	W275K	GCGGCAACCGGCGCAA GAAGGAAGATTGGC (93)	GCAATCTTCTCTTG GCGGGGTGGCGGC (94)	98° for 2' 98° for 30" 50°C for 30" 72° for 11' 40" 72° for 5'

The non-endogenous human GPCRs were then sequenced and the derived and verified nucleic acid and amino acid sequences are listed in the accompanying "Sequence Listing" appendix to this patent document, as summarized in Table F below:

TABLE F

Non Endogenous Human GPCR	Nucleic Acid Sequence Listing	Amino Acid Sequence Listing
hRUP13	SEQ.ID.NO.83	SEQ.ID.NO.84
hRUP14	SEQ.ID.NO.87	SEQ.ID.NO.88
hRUP15	SEQ.ID.NO.91	SEQ.ID.NO.92
hRUP23	SEQ.ID.NO.95	SEQ.ID.NO.96

Example 3 RECEPTOR EXPRESSION

Although a variety of cells are available to the art for the expression of proteins, it is most preferred that mammalian cells be utilized. The primary reason for this is predicated upon practicalities, i.e., utilization of, e.g., yeast cells for the expression of a GPCR, while possible, introduces into the protocol a non-mammalian cell which may not (indeed, in the case of yeast, does not) include the receptor-coupling, genetic-mechanism and secretory pathways that have evolved for mammalian systems - thus, results obtained in non-mammalian cells, while of

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hRUP17	Y215K
hRUP18	L294K
hRUP19	T215K
hRUP20	K248A K248H K248R
hRUP21	K240K
hRUP22	Y222K
hRUP24	A343K
hRUP25	L250K
hRUP26	V253K
hRUP27	T248K

2. QuikChange™ Site-Directed™ Mutagenesis

Preparation of non-endogenous human GPCRs can also be accomplished by using QuikChange™ Site-Directed™ Mutagenesis Kit (Stratagene, according to manufacturer's instructions). Endogenous GPCR is preferably used as a template and two mutagenesis primers utilized, as well as, most preferably, a lysine mutagenesis oligonucleotide and a selection marker oligonucleotide (included in kit). For convenience, the codon mutation incorporated into the novel human GPCR and the respective oligonucleotides are noted, in standard form (Table E):

TABLE E

Receptor Identifier	Codon Mutation	5'-3' orientation (sense), (SEQ.ID.NO.) mutation underlined	5'-3' orientation (antisense) (SEQ.ID.NO.)	Cycle Conditions Min (*), Sec (*) Cycles 2-4 repeated 16 times
hRUP13	A358K	GGGGAGGGGAAAGCAA AGGTGGTCTCTGG (81)	CCAGGAAGAACCACT TTGCTTTGCTCCGC (82)	98° for 2' 98° for 30" 50°C for 30" 72° for 11' 40" 72° for 5'
hRUP14	L246K	CAGGAAGCAAAAGAC CAACATCATCATC (85)	GATGATGATGGTGOT CTTTGCTCTCTGC (86)	98° for 2' 98° for 30" 55°C for 30" 72° for 11' 40" 72° for 5'

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potential use, are not as preferred as that obtained from mammalian cells. Of the mammalian cells, COS-7, 293 and 293T cells are particularly preferred, although the specific mammalian cell utilized can be predicated upon the particular needs of the artisan.

a. Transient Transfection

On day one, 6x10⁶/10 cm dish of 293 cells well were plated out. On day two, two reaction tubes were prepared (the proportions to follow for each tube are per plate): tube A was prepared by mixing 4µg DNA (e.g., pCMV vector; pCMV vector with receptor cDNA, etc.) in 0.5 ml serum free DMEM (Gibco BRL); tube B was prepared by mixing 24µl lipofectamine (Gibco BRL) in 0.5ml serum free DMEM. Tubes A and B were admixed by inversions (several times), followed by incubation at room temperature for 30-45min. The admixture is referred to as the "transfection mixture". Plated 293 cells were washed with 1XPBS, followed by addition of 5 ml serum free DMEM. 1 ml of the transfection mixture were added to the cells, followed by incubation for 4hrs at 37°C/5% CO₂. The transfection mixture was removed by aspiration, followed by the addition of 10ml of DMEM/10% Fetal Bovine Serum. Cells were incubated at 37°C/5% CO₂. After 48hr incubation, cells were harvested and utilized for analysis.

b. Stable Cell Lines: Gs Fusion Protein

Approximately 12x10⁶ 293 cells are plated on a 15cm tissue culture plate. Grown in DME High Glucose Medium containing ten percent fetal bovine serum and one percent sodium pyruvate, L-glutamine, and anti-biotics. Twenty-four hours following plating of 293 cells to ~80% confluency, the cells are transfected using 12µg of DNA. The 12µg of DNA is combined with 60µl of lipofectamine and 2ml of DME High Glucose Medium without serum. The medium is aspirated from the plates and the cells are washed once with medium without serum. The DNA, lipofectamine, and

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medium mixture is added to the plate along with 10mL of medium without serum. Following incubation at 37 degrees Celsius for four to five hours, the medium is aspirated and 25ml of medium containing serum is added. Twenty-four hours following transfection, the medium is aspirated again, and fresh medium with serum is added. Forty-eight hours following transfection, the medium is aspirated and medium with serum is added containing geneticin (G418 drug) at a final concentration of 500µg/mL. The transfected cells now undergo selection for positively transfected cells containing the G418 resistant gene. The medium is replaced every four to five days as selection occurs. During selection, cells are grown to create stable pools, or split for stable clonal selection.

Example 4 ASSAYS FOR DETERMINATION OF CONSTITUTIVE ACTIVITY OF NON-ENDOGENOUS GPCRS

A variety of approaches are available for assessment of constitutive activity of the non-endogenous human GPCRs. The following are illustrative; those of ordinary skill in the art are credited with the ability to determine those techniques that are preferentially beneficial for the needs of the artisan.

1. Membrane Binding Assays: [³⁵S]GTPγS Assay

When a G protein-coupled receptor is in its active state, either as a result of ligand binding or constitutive activation, the receptor couples to a G protein and stimulates the release of GDP and subsequent binding of GTP to the G protein. The alpha subunit of the G protein-receptor complex acts as a GTPase and slowly hydrolyzes the GTP to GDP, at which point the receptor normally is deactivated. Constitutively activated receptors continue to exchange GDP for GTP. The non-hydrolyzable GTP analog, [³⁵S]GTPγS, can be utilized to demonstrate enhanced binding of [³⁵S]GTPγS to membranes expressing constitutively activated receptors. The advantage of using

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antibody. The following serves as a brief protocol for the measurement of changes in cAMP levels in whole cells that express the receptors.

Transfected cells were harvested approximately twenty four hours after transient transfection. Media is carefully aspirated off and discarded. 10ml of PBS is gently added to each dish of cells followed by careful aspiration. 1ml of Sigma cell dissociation buffer and 3ml of PBS are added to each plate. Cells were pipetted off the plate and the cell suspension was collected into a 50ml conical centrifuge tube. Cells were then centrifuged at room temperature at 1,100 rpm for 5 min. The cell pellet was carefully re-suspended into an appropriate volume of PBS (about 3ml/plate). The cells were then counted using a hemocytometer and additional PBS was added to give the appropriate number of cells (with a final volume of about 50 µl/well).

cAMP standards and Detection Buffer (comprising 1 µCi of tracer [¹²⁵I] cAMP (50 µl) to 11 ml Detection Buffer) was prepared and maintained in accordance with the manufacturer's instructions. Assay Buffer was prepared fresh for screening and contained 50µl of Stimulation Buffer, 3µl of test compound (12µM final assay concentration) and 50µl cells. Assay Buffer was stored on ice until utilized. The assay was initiated by addition of 50µl of cAMP standards to appropriate wells followed by addition of 50µl of PBSA to wells H-11 and H12. 50µl of Stimulation Buffer was added to all wells. DMSO (or selected candidate compounds) was added to appropriate wells using a pin tool capable of dispensing 3µl of compound solution, with a final assay concentration of 12µM test compound and 100µl total assay volume. The cells were then added to the wells and incubated for 60 min at room temperature. 100µl of Detection Mix containing tracer cAMP was then added to the wells. Plates were then incubated additional 2 hours followed by counting in a Wallac MicroBeta scintillation

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[³⁵S]GTPγS binding to measure constitutive activation is that: (a) it is generically applicable to all G protein-coupled receptors; (b) it is proximal at the membrane surface making it less likely to pick-up molecules which affect the intracellular cascade.

The assay utilizes the ability of G protein coupled receptors to stimulate [³⁵S]GTPγS binding to membranes expressing the relevant receptors. The assay can, therefore, be used in the direct identification method to screen candidate compounds to known, orphan and constitutively activated G protein-coupled receptors. The assay is generic and has application to drug discovery at all G protein-coupled receptors.

The [³⁵S]GTPγS assay was incubated in 20 mM HEPES and between 1 and about 20mM MgCl₂ (this amount can be adjusted for optimization of results, although 20mM is preferred) pH 7.4, binding buffer with between about 0.3 and about 1.2 nM [³⁵S]GTPγS (this amount can be adjusted for optimization of results, although 1.2 is preferred) and 12.5 to 75 µg membrane protein (e.g. 293 cells expressing the Gs Fusion Protein; this amount can be adjusted for optimization) and 10 µM GDP (this amount can be changed for optimization) for 1 hour. Wheatgerm agglutinin beads (25 µl; Amersham) were then added and the mixture incubated for another 30 minutes at room temperature. The tubes were then centrifuged at 1500 x g for 5 minutes at room temperature and then counted in a scintillation counter.

2. Adenylyl Cyclase

A Flash Plate™ Adenylyl Cyclase kit (New England Nuclear; Cat. No. SMP004A) designed for cell-based assays can be modified for use with crude plasma membranes. The Flash Plate wells can contain a scintillant coating which also contains a specific antibody recognizing cAMP. The cAMP generated in the wells can be quantitated by a direct competition for binding of radioactive cAMP tracer to the cAMP

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counter. Values of cAMP/well were then extrapolated from a standard cAMP curve which was contained within each assay plate.

3. Cell-Based cAMP for Gi Coupled Target GPCRs

TSHR is a Gs coupled GPCR that causes the accumulation of cAMP upon activation. TSHR will be constitutively activated by mutating amino acid residue 623 (i.e., changing an alanine residue to an isoleucine residue). A Gi coupled receptor is expected to inhibit adenylyl cyclase, and, therefore, decrease the level of cAMP production, which can make assessment of cAMP levels challenging. An effective technique for measuring the decrease in production of cAMP as an indication of constitutive activation of a Gi coupled receptor can be accomplished by co-transfecting, most preferably, non-endogenous, constitutively activated TSHR (TSHR-A623I) (or an endogenous, constitutively active Gs coupled receptor) as a "signal enhancer" with a Gi linked target GPCR to establish a baseline level of cAMP. Upon creating a non-endogenous version of the Gi coupled receptor, this non-endogenous version of the target GPCR is then co-transfected with the signal enhancer, and it is this material that can be used for screening. We will utilize such approach to effectively generate a signal when a cAMP assay is used; this approach is preferably used in the direct identification of candidate compounds against Gi coupled receptors. It is noted that for a Gi coupled GPCR, when this approach is used, an inverse agonist of the target GPCR will increase the cAMP signal and an agonist will decrease the cAMP signal.

On day one, 2X10⁶ 293 and 293 cells/well will be plated out. On day two, two reaction tubes will be prepared (the proportions to follow for each tube are per plate): tube A will be prepared by mixing 2µg DNA of each receptor transfected into the mammalian cells, for a total of 4µg DNA (e.g., pCMV vector, pCMV vector with mutated TSHR (TSHR-A623I); TSHR-A623I and GPCR, etc.) in 1.2ml serum free

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DMEM (Irvine Scientific, Irvine, CA); tube B will be prepared by mixing 120µl lipofectamine (Gibco BRL) in 1.2ml serum free DMEM. Tubes A and B will then be admixed by inversions (several times), followed by incubation at room temperature for 30-45min. The admixture is referred to as the "transfection mixture". Plated 293 cells will be washed with 1XPBS, followed by addition of 10ml serum free DMEM. 2.4ml of the transfection mixture will then be added to the cells, followed by incubation for 4hrs at 37°C/5% CO₂. The transfection mixture will then be removed by aspiration, followed by the addition of 25ml of DMEM/10% Fetal Bovine Serum. Cells will then be incubated at 37°C/5% CO₂. After 24hr incubation, cells will then be harvested and utilized for analysis.

A Flash Plate™ Adenyl Cyclase kit (New England Nuclear; Cat. No. SMP004A) is designed for cell-based assays, however, can be modified for use with crude plasma membranes depending on the need of the skilled artisan. The Flash Plate wells will contain a scintillant coating which also contains a specific antibody recognizing cAMP. The cAMP generated in the wells can be quantitated by a direct competition for binding of radioactive cAMP tracer to the cAMP antibody. The following serves as a brief protocol for the measurement of changes in cAMP levels in whole cells that express the receptors.

Transfected cells will be harvested approximately twenty four hours after transient transfection. Media will be carefully aspirated off and discarded. 10ml of PBS will be gently added to each dish of cells followed by careful aspiration. 1ml of Sigma cell dissociation buffer and 3ml of PBS will be added to each plate. Cells will be pipetted off the plate and the cell suspension will be collected into a 50ml conical centrifuge tube. Cells will then be centrifuged at room temperature at 1,100 rpm for 5 min. The cell pellet will be carefully re-suspended into an appropriate volume of PBS (about

200ng of a 8xCRE-Luc reporter plasmid, 50ng of pCMV comprising endogenous receptor or non-endogenous receptor or pCMV alone, and 10ng of a GPRS expression plasmid (GPRS in pcDNA3 (Invitrogen)). The 8xCRE-Luc reporter plasmid was prepared as follows: vector SRIF-β-gal was obtained by cloning the rat somatostatin promoter (-71/+51) at BglV-HindIII site in the pβgal-Basic Vector (Clontech). Eight (8) copies of cAMP response element were obtained by PCR from an adenovirus template AdpCF126CCRE8 (see, *7 Human Gene Therapy* 1883 (1996)) and cloned into the SRIF-β-gal vector at the Kpn-BglV site, resulting in the 8xCRE-β-gal reporter vector. The 8xCRE-Luc reporter plasmid was generated by replacing the beta-galactosidase gene in the 8xCRE-β-gal reporter vector with the luciferase gene obtained from the pGL3-basic vector (Promega) at the HindIII-BamHI site. Following 30 min. incubation at room temperature, the DNA/lipid mixture was diluted with 400 µl of DMEM and 100µl of the diluted mixture was added to each well. 100 µl of DMEM with 10% FCS were added to each well after a 4hr incubation in a cell culture incubator. The following day the transfected cells were changed with 200 µl/well of DMEM with 10% FCS. Eight (8) hours later, the wells were changed to 100 µl /well of DMEM without phenol red, after one wash with PBS. Luciferase activity were measured the next day using the LucLite™ reporter gene assay kit (Packard) following manufacturer instructions and read on a 1450 MicroBeta™ scintillation and luminescence counter (Wallac).

b. AP1 reporter assay (Gq-associated receptors)

A method to detect Gq stimulation depends on the known property of Gq-dependent phospholipase C to cause the activation of genes containing AP1 elements in their promoter. A Pathdetect™ AP-1 cis-Reporting System (Stratagene, Catalogue # 219073) can be utilized following the protocol set forth above with respect to the

3ml/plate). The cells will then be counted using a hemocytometer and additional PBS is added to give the appropriate number of cells (with a final volume of about 50µl/well).

cAMP standards and Detection Buffer (comprising 1 µCi of tracer [¹²⁵I] cAMP (50 µl) to 11 ml Detection Buffer) will be prepared and maintained in accordance with the manufacturer's instructions. Assay Buffer should be prepared fresh for screening and contained 50µl of Stimulation Buffer, 3ul of test compound (12nM final assay concentration) and 50µl cells. Assay Buffer can be stored on ice until utilized. The assay can be initiated by addition of 50µl of cAMP standards to appropriate wells followed by addition of 50µl of PBSA to wells H-11 and H12. 50ul of Stimulation Buffer will be added to all wells. Selected compounds (e.g., TSH) will be added to appropriate wells using a pin tool capable of dispensing 3µl of compound solution, with a final assay concentration of 12µM test compound and 100µl total assay volume. The cells will then be added to the wells and incubated for 60 min at room temperature. 100µl of Detection Mix containing tracer cAMP will then be added to the wells. Plates were then incubated additional 2 hours followed by counting in a Wallac MicroBeta scintillation counter. Values of cAMP/well will then be extrapolated from a standard cAMP curve which is contained within each assay plate.

4. Reporter-Based Assays

a. CRE-LUC Reporter Assay (Gs-associated receptors)

293 and 293T cells are plated-out on 96 well plates at a density of 2×10^4 cells per well and were transfected using Lipofectamine Reagent (BRL) the following day according to manufacturer instructions. A DNA/lipid mixture is prepared for each 6-well transfection as follows: 260ng of plasmid DNA in 100µl of DMEM were gently mixed with 2µl of lipid in 100µl of DMEM (the 260ng of plasmid DNA consisted of

CREB reporter assay, except that the components of the calcium phosphate precipitate were 410 ng pAP1-Luc, 80 ng pCMV-receptor expression plasmid, and 20 ng CMV-SEAP.

c. SRF-LUC Reporter Assay (Gq-associated receptors)

One method to detect Gq stimulation depends on the known property of Gq-dependent phospholipase C to cause the activation of genes containing serum response factors in their promoter. A Pathdetect™ SRF-Luc-Reporting System (Stratagene) can be utilized to assay for Gq coupled activity in, e.g., COS7 cells. Cells are transfected with the plasmid components of the system and the indicated expression plasmid encoding endogenous or non-endogenous GPCR using a Mammalian Transfection™ Kit (Stratagene, Catalogue #200285) according to the manufacturer's instructions. Briefly, 410 ng SRF-Luc, 80 ng pCMV-receptor expression plasmid and 20 ng CMV-SEAP (secreted alkaline phosphatase expression plasmid; alkaline phosphatase activity is measured in the media of transfected cells to control for variations in transfection efficiency between samples) are combined in a calcium phosphate precipitate as per the manufacturer's instructions. Half of the precipitate is equally distributed over 3 wells in a 96-well plate, kept on the cells in a serum free media for 24 hours. The last 5 hours the cells are incubated with 1µM Angiotensin, where indicated. Cells are then lysed and assayed for luciferase activity using a Lucite™ Kit (Packard, Cat. # 6016911) and "TriLux 1450 Microbeta" liquid scintillation and luminescence counter (Wallac) as per the manufacturer's instructions. The data can be analyzed using GraphPad Prism™ 2.0a (GraphPad Software Inc.).

d. Intracellular IP₃ Accumulation Assay (Gq-associated receptors)

On day 1, cells comprising the receptors (endogenous and/or non-endogenous) can be plated onto 24 well plates, usually 1×10^5 cells/well (although this number can be optimized). On day 2 cells can be transfected by firstly mixing 0.25 μ g DNA in 50 μ l serum free DMEM/well and 2 μ l lipofectamine in 50 μ l serumfree DMEM/well. The solutions are gently mixed and incubated for 15-30 min at room temperature. Cells are washed with 0.5 ml PBS and 400 μ l of serum free media is mixed with the transfection media and added to the cells. The cells are then incubated for 3-4 hrs at 37°C/5%CO₂ and then the transfection media is removed and replaced with 1ml/well of regular growth media. On day 3 the cells are labeled with ³H-myo-inositol. Briefly, the media is removed and the cells are washed with 0.5 ml PBS. Then 0.5 ml inositol-free/serum free media (GIBCO BRL) is added/well with 0.25 μ Ci of ³H-myo-inositol/ well and the cells are incubated for 16-18 hrs o/n at 37°C/5%CO₂. On Day 4 the cells are washed with 0.5 ml PBS and 0.45 ml of assay medium is added containing inositol-free/serum free media 10 μ M pargyline 10 mM lithium chloride or 0.4 ml of assay medium and 50 μ l of 10x ketanserin (ket) to final concentration of 10 μ M. The cells are then incubated for 30 min at 37°C. The cells are then washed with 0.5 ml PBS and 200 μ l of fresh/icecold stop solution (1M KOH; 18 mM Na-borate; 3.8 mM EDTA) is added/well. The solution is kept on ice for 5-10 min or until cells were lysed and then neutralized by 200 μ l of fresh/ice cold neutralization sol. (7.5 % HCL). The lysate is then transferred into 1.5 ml eppendorf tubes and 1 ml of chloroform/methanol (1:2) is added/tube. The solution is vortexed for 15 sec and the upper phase is applied to a Biorad AG1-X8™ anion exchange resin (100-200 mesh). Firstly, the resin is washed with water at 1:1.25 W/V and 0.9 ml of upper phase is loaded onto the column. The column is washed with 10 ml of 5 mM myo-inositol and 10 ml of 5 mM Na-borate/60mM Na-formate. The inositol

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tris phosphates are eluted into scintillation vials containing 10 ml of scintillation cocktail with 2 ml of 0.1 M formic acid/ 1 M ammonium formate. The columns are regenerated by washing with 10 ml of 0.1 M formic acid/3M ammonium formate and rinsed twice with dd H₂O and stored at 4°C in water.

Exemplary results are presented below in Table G:

TABLE G

Receptor	Mutation	Assay Utilized (Figure No.)	Signal Generated: CMV	Signal Generated: Endogenous Version (Relative Light Units)	Signal Generated: Non-Endogenous Version (Relative Light Units)	Difference (=) Between CMV v. Wild-type v. Mutant
hRUP12	N/A	IP ₃ (Figure 1)	317.03 cpm/mg protein	3463.29 cpm/mg protein	—	1. 11 Fold
hRUP13	N/A	cAMP (Figure 2)	8.06 pmol/cAMP/mg protein	19.10 pmol/cAMP/mg protein	—	1. 2.4 Fold
	A268K	EXCRE-LUC (Figure 3)	3665.43 LCPS	83280.17 LCPS	61713.6 LCPS	1. 23 Fold
hRUP14	L246K	EXCRE-LUC (Figure 5)	86.07 LCPS	1962.87 LCPS	789.72 LCPS	1. 23 Fold
hRUP15	A398K	EXCRE-LUC (Figure 6)	86.07 LCPS	18286.77 LCPS	17034.83 LCPS	1. 212 Fold
	A398K	cAMP (Figure 7)	15.00 pmol/cAMP/mg protein	164.4 pmol/cAMP/mg protein	117.5 pmol/cAMP/mg protein	1. 11 Fold
hRUP17	N/A	IP ₃ (Figure 9)	317.03 cpm/mg protein	741.07 cpm/mg protein	—	1. 23 Fold
hRUP21	N/A	IP ₃ (Figure 10)	730.5 cpm/mg protein	1421.9 cpm/mg protein	—	1. 2 Fold
hRUP23	W272K	EXCRE-LUC (Figure 11)	311.73 pmol/cAMP/mg protein	13756.00 pmol/cAMP/mg protein	9756.87 pmol/cAMP/mg protein	1. 44 Fold
N/A = not applied						

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Exemplary results of GTPγS assay for detecting constitutive activation, as disclosed in Example 4(1) above, was accomplished utilizing Gs-Fusion Protein Constructs on human RUP13 and RUP15. Table H below lists the signals generated from this assay and the difference in signals as indicated:

TABLE H

Receptor: Gs Fusion Protein	Assay Utilized	Signal Generated: CMV (cpm bound GTP)	Signal Generated: Fusion Protein (cpm bound GTP)	Signal Generated: CMV+ 10 μ M GDP (cpm bound GTP)	Signal Generated: Fusion Protein + 10 μ M GDP (cpm bound GTP)	Difference Between: 1. CMV v. Fusion Protein 2. CMV+GDP vs. Fusion+GDP 3. Fusion vs. Fusion+GDP (cpm bound GTP)
hRUP13-Gs	GTPγS (Figure 4)	32494.0	49351.30	11148.30	28834.67	1. 1.5 Fold
						2. 2.6 Fold
						3. 42%
hRUP15-Gs	GTPγS (Figure 8)	30131.67	32493.67	7697.00	14157.33	1. 1.1 Fold
						2. 1.8 Fold
						3. 56%

Example 5 FUSION PROTEIN PREPARATION

a. GPCR:Gs Fusion Construct

The design of the constitutively activated GPCR-G protein fusion construct was accomplished as follows: both the 5' and 3' ends of the rat G protein Gsα (long form; Itoh, H. et al., 83 *PNAS* 3776 (1986)) were engineered to include a HindIII (5'-AAGCTT-3') sequence thereon. Following confirmation of the correct sequence (including the flanking HindIII sequences), the entire sequence was shuttled into pcDNA3.1(-) (Invitrogen, cat. no. V795-20) by subcloning using the HindIII restriction site of that vector. The correct orientation for the Gsα sequence was determined after

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subcloning into pcDNA3.1(-). The modified pcDNA3.1(-) containing the rat Gsα gene at HindIII sequence was then verified; this vector was now available as a "universal" Gsα protein- vector. The pcDNA3.1(-) vector contains a variety of well-known restriction sites upstream of the HindIII site, thus beneficially providing the ability to insert, upstream of the Gs protein, the coding sequence of an endogenous, constitutively active GPCR. This same approach can be utilized to create other "universal" G protein vectors, and, of course, other commercially available or proprietary vectors known to the artisan can be utilized - the important criteria is that the sequence for the GPCR be upstream and in-frame with that of the G protein.

RUP13 couples via Gs. For the following exemplary GPCR Fusion Proteins, fusion to Gsα was accomplished.

A RUP13-Gsα Fusion Protein construct was made as follows: primers were designed as follows:

5'-gate[TCTAGAAT]GGAGTCTCTCAACCCATCCCCAG-3' (SEQ.ID.NO.37; sense)

15 5'-gate[GATATC]CGTGACTCCAGCCGGGTGAGGCGGC-3' (SEQ.ID.NO.38; antisense).

Nucleotides in lower caps are included as spacers in the restriction sites (designated in brackets) between the G protein and RUP13. The sense and anti-sense primers included the restriction sites for XbaI and EcoRV, respectively, such that spacers (attributed to the restriction sites) exists between the G protein and RUP15.

PCR was then utilized to secure the respective receptor sequences for fusion within the Gsα universal vector disclosed above, using the following protocol for each: 100ng cDNA for RUP15 was added to separate tubes containing 2 μ l of each primer (sense and anti-sense), 3 μ l of 10mM dNTPs, 10 μ l of 10XTaqPlus™ Precision buffer, 1 μ l of TaqPlus™ Precision polymerase (Stratagene: #600211), and 80 μ l of water. Reaction temperatures and cycle times for RUP15 were as follows with cycle steps 2

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through 4 were repeated 35 times: 94°C for 1 min; 94°C for 30 seconds; 62°C for 20 sec; 72°C 1 min 40sec; and 72°C 5 min. PCR product for was run on a 1% agarose gel and then purified (data not shown). The purified product was digested with XbaI and EcoRV and the desired inserts purified and ligated into the Gs universal vector at the respective restriction site. The positive clones was isolated following transformation and determined by restriction enzyme digest; expression using 293 cells was accomplished following the protocol set forth *infra*. Each positive clone for RUP15-Gs Fusion Protein was sequenced to verify correctness. (See, SEQ.ID.NO.:99 for nucleic acid sequence and SEQ.ID.NO.:100 for amino acid sequence).

10 RUP15 couples via Gs. For the following exemplary GPCR Fusion Proteins, fusion to Gs_o was accomplished.

A RUP15-Gs_o Fusion Protein construct was made as follows: primers were designed as follows:

5'-TCTAGAATGAOGTCCACCTGCACCAACAGC-3' (SEQ.ID.NO.:101; sense)

15 5'-gatataGCAGGAAAAGTAGCAGAATOGTAGGAAG-3' (SEQ.ID.NO.:102; antisense).

Nucleotides in lower caps are included as spacers in the restriction sites between the G protein and RUP15. The sense and anti-sense primers included the restriction sites for EcoRV and XbaI, respectively, such that spacers (attributed to the restriction sites) exists between the G protein and RUP15.

20 PCR was then utilized to secure the respective receptor sequences for fusion within the Gs_o universal vector disclosed above, using the following protocol for each: 100ng cDNA for RUP15 was added to separate tubes containing 2μl of each primer (sense and anti-sense), 3μl of 10mM dNTPs, 10μl of 10XTaqPlus™ Precision buffer, 1μl of TaqPlus™ Precision polymerase (Stratagene: #600211), and 80μl of water.

25 Reaction temperatures and cycle times for RUP15 were as follows with cycle steps 2

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for 2 min; 95°C for 20 sec; 56°C for 20 sec; 72°C for 2 min; and 72°C for 7 min. The PCR product will be cloned into a pCRII-TOPO vector (Invitrogen) and sequenced using the ABI Big Dye Terminator kit (P.E. Biosystem). Inserts from a TOPO clone containing the sequence of the fusion construct will be shuttled into the expression vector pcDNA3.1(+) at the HindIII/BamHI site by a 2 step cloning process.

Example 6

TISSUE DISTRIBUTION OF THE DISCLOSED HUMAN GPCRs: RT-PCR

RT-PCR was applied to confirm the expression and to determine the tissue distribution of several novel human GPCRs. Oligonucleotides utilized were GPCR-specific and the human multiple tissue cDNA panels (MTC, Clontech) as templates. Taq DNA polymerase (Stratagene) were utilized for the amplification in a 40μl reaction according to the manufacturer's instructions. 20μl of the reaction will be loaded on a 1.5% agarose gel to analyze the RT-PCR products. Table J below lists the receptors, the cycle conditions and the primers utilized.

TABLE J

Receptor Identifier	Cycle Conditions Min (°), Sec (°) Cycles 2-4 repeated 30 times	5' Primer (SEQ.ID.NO.)	3' Primer (SEQ.ID.NO.)	DNA Fragment	Tissue Expression
hRUF10	94° for 30" 94° for 10" 62°C for 20" 72° for 1" 72° for 7" Cycles 2-4 repeated 35 times	CATGTATGC CAGCGTCT GCTCC (105)	GCTATGCCCTG AAGCGATC TTGTG (106)	720bp	Kidney, leukocyte, liver, placenta and spleen
hRUF11	94° for 2" 94° for 15" 67°C for 15" 72° for 45" 72° for 5"	GCACTCTCT CCTGAGCAC CTTCTCC (107)	CACAGGCTT GCAAGCCCTG CAGCTGCG (108)	630bp	Liver, kidney, pancreas, colon, small intestinal, spleen and prostate

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through 4 were repeated 35 times: 94°C for 1 min; 94°C for 30 seconds; 62°C for 20 sec; 72°C 1 min 40sec; and 72°C 5 min. PCR product for was run on a 1% agarose gel and then purified (data not shown). The purified product was digested with EcoRV and XbaI and the desired inserts purified and ligated into the Gs universal vector at the respective restriction site. The positive clones was isolated following transformation and determined by restriction enzyme digest; expression using 293 cells was accomplished following the protocol set forth *infra*. Each positive clone for RUP15-Gs Fusion Protein was sequenced to verify correctness. (See, SEQ.ID.NO.:103 for nucleic acid sequence and SEQ.ID.NO.:104 for amino acid sequence).

b. Gq(6 amino acid deletion)/Gi Fusion Construct

The design of a Gq (del)/Gi fusion construct can be accomplished as follows: the N-terminal six (6) amino acids (amino acids 2 through 7, having the sequence of TLESIM (SEQ.ID.NO.: 129) Gq_o-subunit will be deleted and the C-terminal five (5) amino acids, having the sequence EYNLV (SEQ.ID.NO.:130) will be replace with the corresponding amino acids of the Gai Protein, having the sequence DCGLP (SEQ.ID.NO.:131). This fusion construct will be obtained by PCR using the following primers:

5'-gatcaagcttcATGGCGTGCTGCTGAGCGAGGAG-3' (SEQ.ID.NO.:132) and

20 5'-gataagcttcTTAGAACAGGCGCAGCTCTTCAGGTTTCAGTGCAGGATGGT-3' (SEQ.ID.NO.:133)

and Plasmid 63313 which contains the mouse Gq_o-wild type version with a 25 hemagglutinin tag as template. Nucleotides in lower caps are included as spacers.

TaqPlus Precision DNA polymerase (Stratagene) will be utilized for the amplification by the following cycles, with steps 2 through 4 repeated 35 times: 95°C

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hRUF12	94° for 2" 94° for 15" 66°C for 15" 72° for 45" 72° for 5"	CCAGTGATG ACTCTGTCC AGCCTG (109)	CAGACACTT GGCAGGGAC GAGGTG (110)	490bp	Brain, colon, heart, kidney, leukocyte, pancreas, prostate, small intestinal, spleen, testis, and thymus
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hRUF13	94° for 1' 94° for 15" 68°C for 20" 72° for 1' 45" 72° for 5'	CTGTGGTCT ACTGCAGCA TGTTCGG (111)	CATATCCCTC CGAGTGTC AGGGCC (112)	700bp	Placenta and lung
hRUF14	94° for 1' 94° for 15" 68°C for 20" 72° for 1' 45" 72° for 5'	ATGGATCCT TATCATGGC TTCTCT (113)	CAAGAACAG GTCTCATCTA AGAGCTCC (114)	700bp	Not yet determined
hRUF16	94° for 30" 94° for 5" 69°C for 15" 72° for 30" 72° for 5'	CTCTGATGC CATCTGCTG GATTCCTG (115)	GTACTGCAC GAAAGTCCA GTGATCC (116)	370bp	Fetal brain, fetal kidney and fetal skeletal muscle
hRUF18	94° for 2' 94° for 15" 60°C for 20" 72° for 1' 72° for 5'	TGGTGGCGA TGGCAACAA GGCTCT (117)	GTTCGGCTT AGGGACAGA TGACC (118)	330bp	Pancreas
hRUF21	94° for 1' 94° for 15" 56°C for 20" 72° for 40" *cycles 2-3 repeated 30 times	TCAACCTGT ATAGCAGCA TCTCT (119)	AAGGAATAG CAGAAATGG TAGCC (120)		Kidney, lung and testis
hRUF22	94° for 30" 94° for 15" 69°C for 20" 72° for 40" *cycles 2-3 repeated 30 times	GACACCTGT CAGCGGTGG TGTGTG (121)	CTGATGGAA GTAGAGGCT GTCCATCTC (122)		Yeast, thymus and spleen
hRUF23	94° for 2' 94° for 15" 60°C for 20" 72° for 1' 72° for 5'	GGGCTGAGC GCAGACCA TGGCTG (123)	CACGGTGAC GAAAGGCAC GAGCTC (124)	530bp	Placenta
hRUF26	94° for 2' 94° for 15" 65°C for 20" 72° for 1' 72° for 5'	AGCATCC TGGCAGGAA GCATGG (125)	CCAGGTAGG TGTGACGCA CAATGTC (126)	470bp	Pancreas
hRUF27	94° for 30" 94° for 10" 55°C for 20" 72° for 1' 72° for 3' *cycles 2-4 repeated 35 times	CTGTTCAC AGGGCTGGT TGGCAAC (127)	ATCATGTCTA GACTCATGGT GATCC (128)	890bp	Brain

PBS, followed by aspiration. Thereafter, 5ml of Membrane Scrape Buffer will be added to scrape cells; this will be followed by transfer of cellular extract into 50ml centrifuge tubes (centrifuged at 20,000 rpm for 17 minutes at 4°C). Thereafter, the supernatant will be aspirated and the pellet will be resuspended in 30ml Membrane Wash Buffer followed by centrifuge at 20,000 rpm for 17 minutes at 4°C. The supernatant will then be aspirated and the pellet resuspended in Binding Buffer. This will then be homogenized using a Brinkman polytron™ homogenizer (15-20 second bursts until the all material is in suspension). This is referred to herein as "Membrane Protein".

2. Bradford Protein Assay

Following the homogenization, protein concentration of the membranes will be determined using the Bradford Protein Assay (protein can be diluted to about 1.5mg/ml, aliquoted and frozen (-80°C) for later use; when frozen, protocol for use will be as follows: on the day of the assay, frozen Membrane Protein is thawed at room temperature, followed by vortex and then homogenized with a polytron at about 12 x 1,000 rpm for about 5-10 seconds; it was noted that for multiple preparations, the homogenizer should be thoroughly cleaned between homogenization of different preparations).

a. Materials

Binding Buffer (as per above); Bradford Dye Reagent; Bradford Protein

Standard will be utilized, following manufacturer instructions (Biorad, cat. no. 500-0006).

b. Procedure

Duplicate tubes will be prepared, one including the membrane, and one as a control "blank". Each contained 800ul Binding Buffer. Thereafter, 10µl of Bradford

Protein Standard (1mg/ml) will be added to each tube, and 10µl of membrane Protein

Example 7

Protocol: Direct Identification of Inverse Agonists and Agonists

A. [³⁵S]GTPγS Assay

Although we have utilized endogenous, constitutively active GPCRs for the direct identification of candidate compounds as, e.g., inverse agonists, for reasons that are not altogether understood, intra-assay variation can become exacerbated. Preferably, then, a GPCR Fusion Protein, as disclosed above, is also utilized with a non-endogenous, constitutively activated GPCR. We have determined that when such a protein is used, intra-assay variation appears to be substantially stabilized, whereby an effective signal-to-noise ratio is obtained. This has the beneficial result of allowing for a more robust identification of candidate compounds. Thus, it is preferred that for direct identification, a GPCR Fusion Protein be used and that when utilized, the following assay protocols be utilized.

1. Membrane Preparation

Membranes comprising the constitutively active orphan GPCR Fusion Protein of interest and for use in the direct identification of candidate compounds as inverse agonists, agonists or partial agonists are preferably prepared as follows:

a. Materials

"Membrane Scrape Buffer" is comprised of 20mM HEPES and 10mM EDTA, pH 7.4; "Membrane Wash Buffer" is comprised of 20 mM HEPES and 0.1 mM EDTA, pH 7.4; "Binding Buffer" is comprised of 20mM HEPES, 100 mM NaCl, and 10 mM MgCl₂, pH 7.4

b. Procedure

All materials will be kept on ice throughout the procedure. Firstly, the media will be aspirated from a confluent monolayer of cells, followed by rinse with 10ml cold

will then be added to just one tube (not the blank). Thereafter, 200ul of Bradford Dye Reagent will be added to each tube, followed by vortex of each. After five (5) minutes, the tubes will be re-vortexed and the material therein will be transferred to cuvettes. The cuvettes will then be read using a CECIL 3041 spectrophotometer, at wavelength 595.

3. Direct Identification Assay

a. Materials

GDP Buffer consisted of 37.5 ml Binding Buffer and 2mg GDP (Sigma, cat. no. G-7127), followed by a series of dilutions in Binding Buffer to obtain 0.2 µM GDP (final concentration of GDP in each well was 0.1 µM GDP); each well comprising a candidate compound, has a final volume of 200ul consisting of 100µl GDP Buffer (final concentration, 0.1µM GDP), 50ul Membrane Protein in Binding Buffer, and 50µl [³⁵S]GTPγS (0.6 nM) in Binding Buffer (2.5 µl [³⁵S]GTPγS per 10ml Binding Buffer).

b. Procedure

Candidate compounds will be preferably screened using a 96-well plate format (these can be frozen at -80°C). Membrane Protein (or membranes with expression vector excluding the GPCR Fusion Protein, as control), will be homogenized briefly until in suspension. Protein concentration will then be determined using the Bradford Protein Assay set forth above. Membrane Protein (and control) will then be diluted to 0.25mg/ml in Binding Buffer (final assay concentration, 12.5µg/well). Thereafter, 100 µl GDP Buffer was added to each well of a Wallac Scintistrip™ (Wallac). A 5ul pin-tool will then be used to transfer 5 µl of a candidate compound into such well (i.e., 5µl in total assay volume of 200 µl is a 1:40 ratio such that the final screening concentration of the candidate compound is 10µM). Again, to avoid contamination, after each transfer step the pin tool should be rinsed in three reservoirs comprising water (1X), ethanol (1X)

and water (2X) - excess liquid should be shaken from the top and each rinse and dried with paper and kimwipes. Thereafter, 50 μ l of Membrane Protein will be added to each well (a control well comprising membranes without the GPCR Fusion Protein was also utilized), and pre-incubated for 5-10 minutes at room temperature. Thereafter, 50 μ l of $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ (0.6 nM) in Binding Buffer will be added to each well, followed by incubation on a shaker for 60 minutes at room temperature (again, in this example, plates were covered with foil). The assay will then be stopped by spinning of the plates at 4000 RPM for 15 minutes at 22°C. The plates will then be aspirated with an 8 channel manifold and sealed with plate covers. The plates will then be read on a Wallace 1450 using setting "Prot. #37" (as per manufacturer instructions).

B. Cyclic AMP Assay

Another assay approach to directly identified candidate compound was accomplished by utilizing a cyclase-based assay. In addition to direct identification, this assay approach can be utilized as an independent approach to provide confirmation of the results from the $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ approach as set forth above.

A modified Flash Plate™ Adenylyl Cyclase kit (New England Nuclear; Cat. No. SMP004A) was preferably utilized for direct identification of candidate compounds as inverse agonists and agonists to constitutively activated orphan GPCRs in accordance with the following protocol.

Transfected cells were harvested approximately three days after transfection. Membranes were prepared by homogenization of suspended cells in buffer containing 20mM HEPES, pH 7.4 and 10mM MgCl_2 . Homogenization was performed on ice using a Brinkman Polytron™ for approximately 10 seconds. The resulting homogenate is centrifuged at 49,000 X g for 15 minutes at 4°C. The resulting pellet was then resuspended in buffer containing 20mM HEPES, pH 7.4 and 0.1 mM EDTA,

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selection of inverse agonists as "leads" from the primary screen involves selection of candidate compounds that that reduce the per cent response by at least the mean plate response, minus two standard deviations. Conversely, an arbitrary preference for selection of an agonists as "leads" from the primary screen involves selection of candidate compounds that increase the per cent response by at least the mean plate response, plus the two standard deviations. Based upon these selection processes, the candidate compounds in the following wells were directly identified as putative inverse agonist (Compound A) and agonist (Compound B) to RUP13 in wells A2 and G9, respectively. See, Figure 12. It is noted for clarity: these compounds have been directly identified without any knowledge of the endogenous ligand for this GPCR. By focusing on assay techniques that are based upon receptor function, and not compound binding affinity, we are able to ascertain compounds that are able to reduce the functional activity of this receptor (Compound A) as well as increase the functional activity of the receptor (Compound B). Based upon the location of these receptor in lung tissue (see, for example, hRUP13 and hRUP21 in Example 6), pharmaceutical agents can be developed for potential therapeutic treatment of lung cancer.

References cited throughout this patent document, including co-pending and related patent applications, unless otherwise indicated, are fully incorporated herein by reference. Modifications and extension of the disclosed inventions that are within the purview of the skilled artisan are encompassed within the above disclosure and the claims that follow.

Although a variety of expression vectors are available to those in the art, for purposes of utilization for both the endogenous and non-endogenous human GPCRs, it is most preferred that the vector utilized be pCMV. This vector was deposited with the American Type Culture Collection (ATCC) on October 13, 1998 (10801 University

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homogenized for 10 seconds, followed by centrifugation at 49,000 X g for 15 minutes at 4°C. The resulting pellet was then stored at -80°C until utilized. On the day of direct identification screening, the membrane pellet as slowly thawed at room temperature, resuspended in buffer containing 20mM HEPES, pH 7.4 and 10mM MgCl_2 , to yield a final protein concentration of 0.60mg/ml (the resuspended membranes are placed on ice until use).

cAMP standards and Detection Buffer (comprising 2 μ Ci of tracer $[^{125}\text{I}]$ cAMP (100 μ l) to 11 ml Detection Buffer) were prepared and maintained in accordance with the manufacturer's instructions. Assay Buffer was prepared fresh for screening and contained 20mM HEPES, pH 7.4, 10mM MgCl_2 , 20mM phosphocreatine (Sigma), 0.1 units/ml creatine phosphokinase (Sigma), 50 μ M GTP (Sigma), and 0.2 mM ATP (Sigma); Assay Buffer was then stored on ice until utilized.

Candidate compounds identified as per above (if frozen, thawed at room temperature) were added, preferably, to 96-well plate wells (3 μ l/well; 12 μ M final assay concentration), together with 40 μ l Membrane Protein (30 μ g/well) and 50 μ l of Assay Buffer. This admixture was then incubated for 30 minutes at room temperature, with gentle shaking.

Following the incubation, 100 μ l of Detection Buffer was added to each well, followed by incubation for 2-24 hours. Plates were then counted in a Wallace MicroBeta™ plate reader using "Prot. #31" (as per manufacturer instructions).

A representative screening assay plate (96 well format) result is presented in Figure 12. Each bar represents the results for a different compound in each well, plus RUP13-Gsc Fusion Protein construct, as prepared in Example 5(a) above. The representative results presented in Figure 12 also provide standard deviations based upon the mean results of each plate ("m") and the mean plus two arbitrary preference for

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Blvd., Manassas, VA 20110-2209 USA) under the provisions of the Budapest Treaty for the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure. The DNA was tested by the ATCC and determined to be viable. The ATCC has assigned the following deposit number to pCMV: ATCC #203351.

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CLAIMS

What is claimed is:

1. A G protein-coupled receptor encoded by an amino acid sequence of SEQ.ID.NO.:2.
2. A non-endogenous, constitutively activated version of the G protein-coupled receptor of claim 1.
3. A plasmid comprising a vector and the cDNA of SEQ.ID.NO.:1.
4. A host cell comprising the plasmid of claim 3.
5. A G protein-coupled receptor encoded by an amino acid sequence of SEQ.ID.NO.:4.
6. A non-endogenous, constitutively activated version of the G protein-coupled receptor of claim 5.
7. A plasmid comprising a vector and the cDNA of SEQ.ID.NO.:3.
8. A host cell comprising the plasmid of claim 7.
9. A G protein-coupled receptor encoded by an amino acid sequence of SEQ.ID.NO.:6.
10. A non-endogenous, constitutively activated version of the G protein-coupled receptor of claim 9.
11. A plasmid comprising a vector and the cDNA of SEQ.ID.NO.:5.
12. A host cell comprising the plasmid of claim 11.
13. A G protein-coupled receptor encoded by an amino acid sequence of SEQ.ID.NO.:8.
14. A non-endogenous, constitutively activated version of the G protein-coupled receptor of claim 13.

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32. A host cell comprising the plasmid of claim 31.
33. A G protein-coupled receptor encoded by an amino acid sequence of SEQ.ID.NO.:18.
34. A non-endogenous, constitutively activated version of the G protein-coupled receptor of claim 33.
35. A plasmid comprising a vector and the cDNA of SEQ.ID.NO.:17.
36. A host cell comprising the plasmid of claim 35.
37. A G protein-coupled receptor encoded by an amino acid sequence of SEQ.ID.NO.:20.
38. A non-endogenous, constitutively activated version of the G protein-coupled receptor of claim 37.
39. A plasmid comprising a vector and the cDNA of SEQ.ID.NO.:19.
40. A host cell comprising the plasmid of claim 39.
41. A G protein-coupled receptor encoded by an amino acid sequence of SEQ.ID.NO.:22.
42. A non-endogenous, constitutively activated version of the G protein-coupled receptor of claim 41.
43. A plasmid comprising a vector and the cDNA of SEQ.ID.NO.:21.
44. A host cell comprising the plasmid of claim 43.
45. A G protein-coupled receptor encoded by an amino acid sequence of SEQ.ID.NO.:24.
46. A non-endogenous, constitutively activated version of the G protein-coupled receptor of claim 45.
47. A plasmid comprising a vector and the cDNA of SEQ.ID.NO.:23.
48. A host cell comprising the plasmid of claim 47.

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15. A plasmid comprising a vector and the cDNA of SEQ.ID.NO.:7.
16. A host cell comprising the plasmid of claim 15.
17. A G protein-coupled receptor encoded by an amino acid sequence of SEQ.ID.NO.:10.
18. A non-endogenous, constitutively activated version of the G protein-coupled receptor of claim 17.
19. A plasmid comprising a vector and the cDNA of SEQ.ID.NO.:9.
20. A host cell comprising the plasmid of claim 19.
21. A G protein-coupled receptor encoded by an amino acid sequence of SEQ.ID.NO.:12.
22. A non-endogenous, constitutively activated version of the G protein-coupled receptor of claim 21 comprising an amino acid sequence of SEQ.ID.NO.:84.
23. A plasmid comprising a vector and the cDNA of SEQ.ID.NO.:11.
24. A host cell comprising the plasmid of claim 23.
25. A G protein-coupled receptor encoded by an amino acid sequence of SEQ.ID.NO.:14.
26. A non-endogenous, constitutively activated version of the G protein-coupled receptor of claim 25 comprising an amino acid sequence of SEQ.ID.NO.:88.
27. A plasmid comprising a vector and the cDNA of SEQ.ID.NO.:13.
28. A host cell comprising the plasmid of claim 27.
29. A G protein-coupled receptor encoded by an amino acid sequence of SEQ.ID.NO.:16.
30. A non-endogenous, constitutively activated version of the G protein-coupled receptor of claim 29 comprising an amino acid sequence of SEQ.ID.NO.:92.
31. A plasmid comprising a vector and the cDNA of SEQ.ID.NO.:15.

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49. A G protein-coupled receptor encoded by an amino acid sequence of SEQ.ID.NO.:26.
50. A non-endogenous, constitutively activated version of the G protein-coupled receptor of claim 49.
51. A plasmid comprising a vector and the cDNA of SEQ.ID.NO.:25.
52. A host cell comprising the plasmid of claim 51.
53. A G protein-coupled receptor encoded by an amino acid sequence of SEQ.ID.NO.:28.
54. A non-endogenous, constitutively activated version of the G protein-coupled receptor of claim 53.
55. A plasmid comprising a vector and the cDNA of SEQ.ID.NO.:27.
56. A host cell comprising the plasmid of claim 55.
57. A G protein-coupled receptor encoded by an amino acid sequence of SEQ.ID.NO.:30.
58. A non-endogenous, constitutively activated version of the G protein-coupled receptor of claim 57.
59. A plasmid comprising a vector and the cDNA of SEQ.ID.NO.:29.
60. A host cell comprising the plasmid of claim 59.
61. A G protein-coupled receptor encoded by an amino acid sequence of SEQ.ID.NO.:32.
62. A non-endogenous, constitutively activated version of the G protein-coupled receptor of claim 61 comprising an amino acid sequence of SEQ.ID.NO.:96.
63. A plasmid comprising a vector and the cDNA of SEQ.ID.NO.:95.
64. A host cell comprising the plasmid of claim 63.

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65. A G protein-coupled receptor encoded by an amino acid sequence of
SEQ.ID.NO.:34.

66. A non-endogenous, constitutively activated version of the G protein-coupled
receptor of claim 65.

67. A plasmid comprising a vector and the cDNA of SEQ.ID.NO.:33.

68. A host cell comprising the plasmid of claim 67.

69. A G protein-coupled receptor encoded by an amino acid sequence of
SEQ.ID.NO.:36.

70. A non-endogenous, constitutively activated version of the G protein-coupled
receptor of claim 69.

71. A plasmid comprising a vector and the cDNA of SEQ.ID.NO.:35.

72. A host cell comprising the plasmid of claim 71.

73. A G protein-coupled receptor encoded by an amino acid sequence of
SEQ.ID.NO.:38.

74. A non-endogenous, constitutively activated version of the G protein-coupled
receptor of claim 73.

75. A plasmid comprising a vector and the cDNA of SEQ.ID.NO.:37.

76. A host cell comprising the plasmid of claim 75.

77. A G protein-coupled receptor encoded by an amino acid sequence of
SEQ.ID.NO.:40.

78. A non-endogenous, constitutively activated version of the G protein-coupled
receptor of claim 77.

79. A plasmid comprising a vector and the cDNA of SEQ.ID.NO.:39.

80. A host cell comprising the plasmid of claim 79.

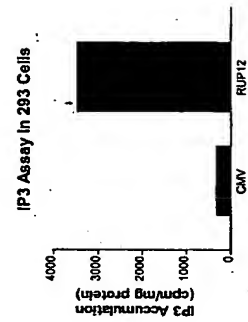


Figure 1

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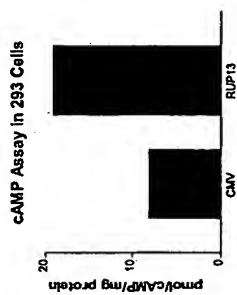


Figure 2

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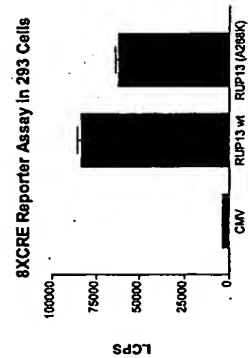


Figure 3

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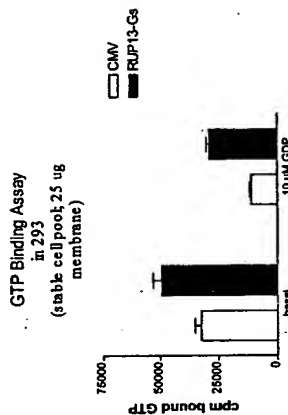


Figure 4

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8XCRE Reporter Assay in 293 Cells

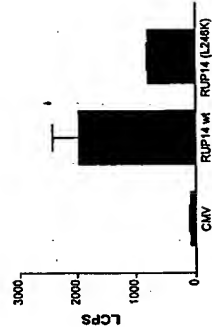


Figure 5

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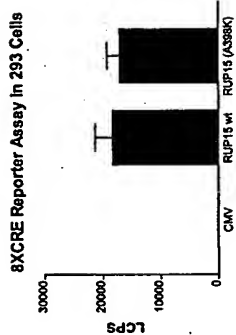


Figure 6

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cAMP Assay in 293 Cells



Figure 7

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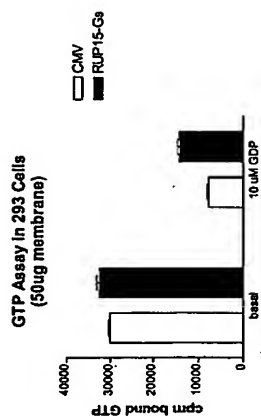


Figure 8

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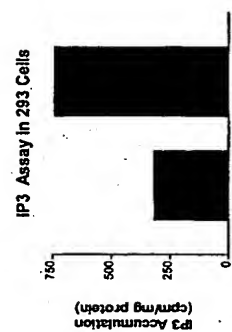


Figure 9

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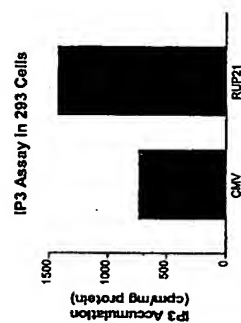


Figure 10

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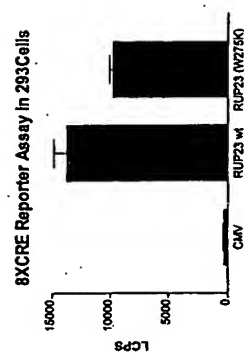


Figure 11

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SEQUENCE LISTING

<110> Arena Pharmaceuticals, Inc.
 Chan, Ruyong
 Dang, Huong T.
 Lowitz, Kevin P.

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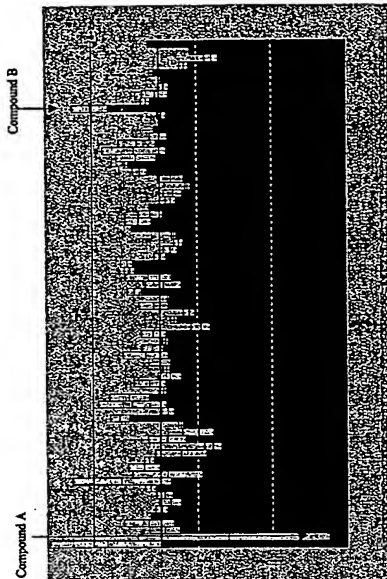


Figure 12

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Page 3

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Page 5

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235 240 245
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255 260 265
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275 280 285
Arg Val Gly Thr Lys Pro Ser Ala Ser Leu Arg Trp His Gln Ala Leu 290
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315 320 325
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375 380 385
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415 420 423
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Page 9

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 35 40 45

Met Leu Leu Leu Asp Leu Thr Ala Val Ala Gly An Ala Ala Val Met
 50 55 60

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Ala Val Ile Ala Lys Thr Pro Ala Leu Arg Lys Phe Val Phe Val Phe
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 His Leu Cys Leu Val Asp Leu Leu Ala Leu Thr Leu Met Pro Leu
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 Val Ala Cys Arg Leu Tyr Leu Phe Leu Ser Val Cys Phe Val Ser Leu
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 Ala Ile Leu Ser Val Ser Ala Ile An Val Glu Arg Tyr Tyr Val
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 Val His Pro Met Arg Tyr Glu Val Arg Met Thr Leu Gly Leu Val Ala
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 Ser Val Leu Val Gly Val Trp Val Lys Ala Leu Ala Met Ala Ser Val
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 Pro Gly Cys Ser Leu Gln Trp Ser His Ser Ala Tyr Cys Gln Leu Phe
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 Val Val Val Phe Ala Val Leu Tyr Phe Leu Leu Pro Leu Leu Ile
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 Leu Val Val Tyr Cys Ser Met Phe Arg Val Ala Arg Val Ala Met
 225 230 235 240
 Gln His Gly Pro Leu Pro Thr Trp Met Glu Thr Pro Arg Gln Arg Ser
 245 250 255
 Glu Ser Leu Ser Ser Arg Ser Thr Met Val Thr Ser Ser Gly Ala Pro
 260 265 270
 Gln Thr Thr Pro His Arg Thr Phe Gly Gly Gly Lys Ala Ala Val
 275 280 285
 Leu Leu Ala Val Gly Gly Gln Phe Leu Leu Cys Trp Leu Pro Tyr Phe
 290 295 300
 Ser Phe His Leu Tyr Val Ala Leu Ser Ala Gln Pro Ile Ser Thr Gly
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 325 330 335
 An Pro Phe Phe Tyr Gly Cys Leu An Arg Gln Ile Arg Gly Glu Leu
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 Ser Lys Gln Phe Val Cys Phe Phe Lys Pro Ala Pro Glu Glu Leu
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 Arg Leu Pro Ser Arg Glu Gly Ser Ile Glu Glu An Phe Leu Gln Phe
 370 375 380
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 Pro Ser Pro Lys Gln Glu Pro Pro Ala Val Asp Phe Arg Ile Pro Gly
 405 410 415

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Gln Ile Ala Glu Glu Thr Ser Glu Phe Leu Glu Gln Gln Leu Thr Ser
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Page 14

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 Phe Phe Trp Gly Val Leu Gly An Gly Leu Ser Ile Tyr Val Phe Leu
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 Gln Pro Tyr Lys Lys Ser Thr Ser Val An Val Phe Met Leu An Leu
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 130 135 140
 Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly
 145 150 155 160
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Page 18

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 340 345 350
 355 360

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275 280 285
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 Gln Leu Leu His Lys His Gln Arg Lys Ser Ile Phe Lys Ile Lys Lys
 305 310 315 320
 Lys Ser Leu Ser Thr Ser Ile Val Trp Ile Glu Asp Ser Ser Ser Leu
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 Gly Ala Pro Ala Ser Gly Pro Pro Ser Arg Arg Val Arg Leu Val Phe
 35 40 45

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Leu Gly Val Ile Leu Val Val Ala Val Ala Gly Asn Thr Thr Val Leu
 50 55 60
 Cys Arg Leu Cys Gly Gly Gly Gly Pro Trp Ala Gly Pro Lys Arg Arg
 65 70 75 80
 Lys Met Asp Phe Leu Leu Val Gln Leu Ala Leu Ala Asp Leu Tyr Ala
 85 90 95
 Cys Gly Gly Thr Ala Leu Ser Gln Leu Ala Trp Glu Leu Leu Gly Gly
 100 105 110
 Pro Arg Ala Ala Thr Gly Asp Leu Ala Cys Arg Phe Leu Gln Leu Leu
 115 120 125
 Gln Ala Ser Gly Arg Gly Ala Ser Ala His Leu Val Val Leu Ile Ala
 130 135 140
 Leu Glu Arg Arg Arg Ala Val Arg Leu Pro His Gly Arg Pro Leu Pro
 145 150 155 160
 Ala Arg Ala Leu Ala Ala Leu Gly Trp Leu Leu Ala Leu Leu Ala
 165 170 175
 Leu Pro Pro Ala Phe Val Val Arg Gly Asp Ser Pro Ser Pro Leu Pro
 180 185 190
 Pro Pro Pro Pro Thr Ser Leu Gln Pro Gly Ala Pro Pro Ala Ala
 195 200 205
 Arg Ala Trp Pro Gly Glu Arg Arg Cys His Gly Ile Phe Ala Pro Leu
 210 215 220
 Pro Arg Trp His Leu Gln Val Tyr Ala Phe Tyr Glu Ala Val Ala Gly
 225 230 235 240
 Phe Val Ala Pro Val Thr Val Leu Gly Val Ala Cys Gly His Leu Leu
 245 250 255
 Ser Val Trp Trp Arg His Arg Pro Gln Ala Pro Ala Ala Ala Pro
 260 265 270
 Trp Ser Ala Ser Pro Gly Arg Ala Pro Ala Pro Ser Ala Leu Pro Arg
 275 280 285
 Ala Lys Val Gln Ser Leu Lys Met Ser Leu Leu Leu Ala Leu Leu Phe
 290 295 300
 Val Gly Cys Glu Leu Pro Tyr Phe Ala Ala Arg Leu Ala Ala Trp
 305 310 315 320
 Ser Ser Gly Pro Ala Gly Asp Trp Glu Gly Glu Gly Leu Ser Ala Ala
 325 330 335
 Leu Arg Val Val Ala Met Asn Ser Ala Leu Asn Pro Phe Val Tyr
 340 345 350
 Leu Phe Phe Gln Ala Gly Asp Cys Arg Leu Arg Arg Gln Leu Arg Lys
 355 360 365
 Arg Leu Gly Ser Leu Cys Cys Ala Pro Gln Gly Gly Ala Glu Asp Glu
 370 375 380
 Glu Gly Pro Arg Gly His Gln Ala Leu Tyr Arg Gln Arg Trp Pro His
 385 390 395 400

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Pro His Tyr His His Ala Arg Arg Glu Pro Leu Asp Glu Gly Gly Leu
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Arg Pro Pro Pro Pro Arg Pro Arg Pro Leu Pro Cys Ser Cys Glu Ser
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Ala Phe
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<212> DNA
<213> Homo sapiens
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<211> 346
<212> PRT
<213> Homo sapiens

<400> 24
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20 25 30
Page 24

Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
35 40 45
Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
50 55 60
Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
65 70 75 80
Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Thr Thr Leu Ala
85 90 95
Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp
100 105 110
Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser
115 120 125
Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
130 135 140
Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu
145 150 155 160
Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
165 170 175
His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile
180 185 190
Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln
195 200 205
Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val
210 215 220
Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg
225 230 235 240
Leu Tyr Phe Leu Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val
245 250 255
His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
260 265 270
Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe
275 280 285
Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His
290 295 300
Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg
305 310 315 320
Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly
325 330 335
Gln Trp Asp Pro His Ile Val Glu Trp His
340 345

<210> 25
<211> 1011
<212> DNA
<213> Homo sapiens

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aacttactg tgcagctgc cctgctttt atgagtatct attctcga agttttcaa 240
tgggaatgc aactgttcca atgcagatg gtcaatttc tgggaactct atcatgcat 300
gcaagtatg tgcagctct cttaatttta agttgagtg cctacagcc ctatgctacc 360
ttaagcaaa aggtttcttc gcaagagact acttcatgct atgagaat attttatgg 420
cattactga aaaaatttgc ccagcccaac ttgtctgaaa aactgtcat tcatatgg 480
ggagtgtac tgggcaaat cacttcaggt accgtatcat actcagcat agagctaca 540
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atgcaggtc tcatggaac cacatttatt ggttttctt ttttatagt actaacaca 660
tactactct ttgaagcca tctgaaaaa atagaaacct gtagctcat tatggagaa 720
gatttgactt acagttctgt gaaagacat cttttgttca tccapcttt actaatgtt 780
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<211> 336
<212> PRT
<213> Homo sapiens

<400> 26
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Asn Thr Leu Ser Gln Trp Ile Phe Leu Thr Lys Ile Gly Lys Lys Thr
35 40 45
Ser Thr His Ile Tyr Leu Ser His Leu Val Thr Ala Asn Leu Leu Val
50 55 60
Cys Ser Ala Met Pro Phe Met Ser Ile Tyr Phe Leu Lys Gly Phe Gln
65 70 75 80
Trp Glu Tyr Gln Ser Ala Gln Cys Arg Val Val Asn Phe Leu Gly Thr
85 90 95
Leu Ser Met His Ala Ser Met Phe Val Ser Leu Leu Ile Leu Ser Trp
100 105 110

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Ile Ala Ile Ser Arg Tyr Ala Thr Leu Met Gln Lys Asp Ser Ser Gln
115 120 125
Glu Thr Thr Ser Cys Tyr Glu Lys Ile Phe Tyr Gly His Leu Leu Lys
130 135 140
Lys Phe Arg Gln Pro Asn Phe Ala Arg Lys Leu Cys Ile Tyr Ile Trp
145 150 155 160
Gly Val Val Leu Gly Ile Ile Ile Pro Val Thr Val Tyr Ser Val
165 170 175
Ile Glu Ala Thr Glu Gly Glu Glu Ser Leu Cys Tyr Asn Arg Gln Met
180 185 190
Glu Leu Gly Ala Met Ile Ser Gln Ile Ala Gly Leu Ile Gly Thr Thr
195 200 205
Phe Ile Gly Phe Ser Phe Leu Val Val Leu Thr Ser Tyr Tyr Ser Phe
210 215 220
Val Ser His Leu Arg Lys Ile Arg Thr Cys Thr Ser Ile Met Glu Lys
225 230 235 240
Asp Leu Thr Tyr Ser Ser Val Lys Arg His Leu Leu Val Ile Gln Ile
245 250 255
Leu Leu Ile Val Cys Phe Leu Pro Tyr Ser Ile Phe Lys Pro Ile Phe
260 265 270
Tyr Val Leu His Gln Arg Asp Asn Cys Gln Gln Leu Asn Tyr Leu Ile
275 280 285
Glu Thr Lys Asn Ile Leu Thr Cys Leu Ala Ser Ala Arg Ser Ser Thr
290 295 300
Asp Pro Ile Ile Phe Leu Leu Leu Asp Lys Thr Phe Lys Lys Thr Leu
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Tyr Asn Leu Phe Thr Lys Ser Asn Ser Ala His Met Gln Ser Tyr Gly
325 330 335

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<212> DNA
<213> Homo sapiens

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aaatgagac cttggaagag cagccacatc attactgta accgtgctg cagactgtg 240
ctgtatctga ccagctcccc cttctgatt cactactatg cagtggtgca aaactgttc 300
tttgaattt tcatgtgaa gtttatccg ttacgttcc attcaactt gtagacaga 360
atctcttccc tcaactgttt cagacttccc cgtctatgtg tgaatcttca ccaactgagc 420
tgcctttccc ttcacaaac tgaatgtgca gttgtagctt gttggtgtt gttgactt 480
tcaatgttag ctgtacttcc gatgacttcc ttgatccat caacacag gacacaga 540

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tcagctgtc tcagctgtc cagctgtc gaactcaat ctattagtg gtacacctg 600
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 aggtacaa ttctgtact ccttgacttt tacytatgt tttaccctt ccatatctg 780
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<210> 28
 <211> 337
 <212> PRT
 <213> Homo sapiens

<400> 28

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Tyr Ala Ala Ala Phe Gly Asn Cys Thr Asp Glu Asn Ile Pro Leu Lys 20 25 30

Met His Tyr Leu Pro Val Ile Tyr Gly Ile Ile Phe Leu Val Gly Phe 35 40 45

Pro Gly Asn Ala Val Val Ile Ser Thr Tyr Ile Phe Lys Met Arg Pro 50 55 60

Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Cys Thr Asp Leu 65 70 75 80

Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly 85 90 95

Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Ser 100 105 110

Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser 115 120 125

Ile Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile 130 135 140

His Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile 145 150 155 160

Ser Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn 165 170 175

Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Gly Leu 180 185 190

Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys 195 200 205

Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile His Thr 210 215 220

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<210> 30
 <211> 330
 <212> PRT
 <213> Homo sapiens

<400> 30

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Gly Asn Asp Glu Ala Leu Leu Leu Cys Gly Lys Glu Thr Leu Ile 20 25 30

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Gly Phe Val Leu Trp Leu Leu Gly Phe Arg Met Arg Arg Asn Ala Phe 50 55 60

Ser Val Tyr Val Leu Ser Leu Ala Gly Ala Asp Phe Leu Phe Leu Cys 65 70 75 80

Phe Glu Ile Ile Asn Cys Leu Val Tyr Leu Ser Asn Phe Phe Cys Ser 85 90 95

Ile Ser Ile Asn Phe Pro Ser Phe Phe Thr Thr Val Met Thr Cys Ala 100 105 110

Tyr Leu Ala Gly Leu Ser Met Leu Ser Thr Val Ser Thr Glu Arg Cys 115 120 125

Leu Ser Val Leu Trp Pro Ile Trp Tyr Arg Cys Arg Pro Arg His 130 135 140

Leu Ser Ala Val Val Cys Val Leu Leu Trp Ala Leu Ser Leu Leu Leu 145 150 155 160

Ser Ile Leu Glu Gly Lys Phe Cys Gly Phe Leu Phe Ser Asp Gly Asp 165 170 175

Ser Gly Trp Cys Glu Thr Phe Asp Phe Ile Thr Ala Ala Trp Leu Ile 180 185 190

Phe Leu Phe Met Val Leu Cys Gly Ser Ser Leu Ala Leu Leu Val Arg 195 200 205

Ile Leu Cys Gly Ser Arg Gly Leu Pro Leu Thr Arg Leu Tyr Leu Thr 210 215 220

Ile Leu Leu Thr Val Leu Val Phe Leu Leu Cys Gly Leu Pro Phe Gly 225 230 235 240

Ile Glu Trp Phe Leu Ile Leu Trp Ile Trp Lys Asp Ser Asp Val Leu 245 250 255

Phe Cys His Ile His Pro Val Ser Val Val Leu Ser Ser Leu Asn Ser 260 265 270

Ser Ala Asn Pro Ile Ile Tyr Phe Phe Val Gly Ser Phe Arg Lys Glu 275 280 285

Trp Arg Leu Glu Gln Pro Ile Leu Lys Leu Ala Leu Glu Arg Ala Leu 290 295 300

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210 215 220
 Leu Thr His Gly Leu Glu Thr Asp Ser Cys Leu Lys Glu Lys Ala Arg 225 235 240
 Arg Leu Thr Ile Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro 245 255
 Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile 260 270
 Ser Cys Ser Ile Glu Asn Glu Ile His Glu Ala Tyr Ile Val Ser Arg 275 285
 Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Tyr Val Val 290 300
 Val Ser Asp Asn Phe Glu Glu Ala Val Cys Ser Thr Val Arg Cys Lys 305 315 320
 Val Ser Gly Asn Leu Glu Glu Ala Lys Lys Ile Ser Tyr Ser Asn Asn 325 335

Pro

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 <211> 993
 <212> DNA
 <213> Homo sapiens

<400> 29

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 cagaggtct tgcagacat tctgaggtg gatcaggtg aaggtgctt cctgacggc 960
 accccggga tgtcagagc cagttggtg tag 993

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Glu Asp Ile Ala Glu Val Asp His Ser Glu Gly Cys Phe Arg Glu Glu 305 310 315 320
 Thr Pro Glu Met Ser Arg Ser Ser Leu Val 325 330

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 <211> 1092
 <212> DNA
 <213> Homo sapiens

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 <211> 343
 <212> PRT
 <213> Homo sapiens

<400> 32

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35 40 45
Ser Leu Gly His Leu Leu Ala Ala Leu Asp Met Pro Phe Thr Leu
50 55 60
Leu Gly Val Met Arg Gly Arg Thr Pro Ser Ala Pro Gly Ala Cys Gln
65 70 75 80
Val Ile Gly Phe Leu Asp Thr Phe Leu Ala Ser Asn Ala Ala Leu Ser
85 90 95
Val Ala Ala Leu Ser Ala Asp Gln Trp Leu Ala Val Gly Phe Pro Leu
100 105 110
Arg Tyr Ala Gly Arg Leu Arg Pro Arg Tyr Ala Gly Leu Leu Gly
115 120 125
Cys Ala Trp Gly Gln Ser Leu Ala Phe Ser Gly Ala Ala Leu Gly Cys
130 135 140
Ser Trp Leu Gly Tyr Ser Ser Ala Phe Ala Ser Cys Ser Leu Arg Leu
145 150 155 160
Pro Pro Gln Pro Gln Arg Pro Arg Phe Ala Ala Phe Thr Ala Thr Leu
165 170 175
His Ala Val Gly Phe Val Leu Pro Leu Ala Val Leu Cys Leu Thr Ser
180 185 190
Leu Gln Val His Arg Val Ala Arg Ser His Cys Gln Arg Met Asp Thr
195 200 205
Val Thr Met Lys Ala Leu Ala Leu Leu Ala Asp Leu His Pro Ser Val
210 215 220
Arg Gln Arg Cys Leu Ile Gln Gln Lys Arg Arg Arg His Arg Ala Thr
225 230 235 240
Arg Lys Ile Gly Ile Ala Ile Ala Thr Phe Leu Ile Cys Phe Ala Pro
245 250 255
Tyr Val Met Thr Arg Leu Ala Glu Leu Val Pro Phe Val Thr Val Asn
260 265 270
Ala Gln Trp Gly Ile Leu Ser Lys Cys Leu Thr Tyr Ser Lys Ala Val
275 280 285
Ala Asp Pro Phe Thr Tyr Ser Leu Leu Arg Arg Pro Phe Arg Gln Val
290 295 300
Leu Ala Gly Met Val His Arg Leu Leu Lys Arg Thr Pro Arg Pro Ala
305 310 315 320
Ser Thr His Asp Ser Ser Leu Asp Val Ala Gly Met Val His Gln Leu
325 330 335
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Thr Glu Asn Asp Ser Cys Leu Gln Gln Thr His
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<210> 33
<211> 1125

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<212> DNA
<213> Homo sapiens
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<212> PRT
<213> Homo sapiens
<400> 34

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35 40 45
Val Gly Ala Ile Gly Leu Leu Gly Asn Leu Ala Val Leu Trp Val Leu
50 55 60
Ser Asn Cys Ala Arg Ala Pro Gly Pro Pro Ser Asp Thr Phe Val
65 70 75 80

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Phe Asn Leu Ala Leu Ala Asp Leu Gly Leu Ala Leu Thr Leu Pro Phe
85 90 95
Trp Ala Ala Gln Ser Ala Leu Asp Phe His Trp Pro Phe Gly Gly Ala
100 105 110
Leu Cys Lys Met Val Leu Thr Ala Thr Val Leu Asn Val Tyr Ala Ser
115 120 125
Ile Phe Leu Ile Thr Ala Leu Ser Val Ala Arg Tyr Trp Val Val Ala
130 135 140
Met Ala Ala Gly Pro Gly Thr His Leu Ser Leu Phe Trp Ala Arg Ile
145 150 155 160
Ala Thr Leu Ala Val Trp Ala Ala Ala Leu Val Thr Val Thr Thr
165 170 175
Ala Val Phe Gly Val Gln Gly Gln Val Cys Gly Val Arg Leu Cys Leu
180 185 190
Leu Arg Phe Pro Ser Arg Tyr Trp Leu Gly Ala Tyr Gln Leu Gln Arg
195 200 205
Val Val Leu Ala Phe Met Val Pro Leu Gly Val Ile Thr Thr Ser Tyr
210 215 220
Leu Leu Leu Leu Ala Phe Leu Gln Arg Arg Gln Arg Arg Gln Asp
225 230 235 240
Ser Arg Val Val Ala Arg Ser Val Arg Ile Leu Val Ala Ser Phe Phe
245 250 255
Leu Cys Trp Phe Pro Asn His Val Val Thr Leu Trp Gly Val Leu Val
260 265 270
Lys Phe Asp Leu Val Pro Trp Asn Ser Thr Phe Tyr Thr Ile Gln Thr
275 280 285
Tyr Val Phe Pro Val Thr Thr Cys Leu Ala His Ser Asn Ser Cys Leu
290 295 300
Asn Pro Val Leu Tyr Cys Leu Leu Arg Arg Gln Pro Arg Gln Ala Leu
305 310 315 320
Ala Gly Thr Phe Arg Asp Leu Arg Ser Arg Leu Trp Pro Gln Gly Gly
325 330 335
Gly Trp Val Gln Gln Val Ala Leu Lys Gln Val Gly Arg Arg Trp Val
340 345 350
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Asp Arg Gly Thr Pro Gly
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<211> 1092
<212> DNA
<213> Homo sapiens

<400> 35
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<212> PRT
<213> Homo sapiens
<400> 36

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20 25 30
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35 40 45
Leu Trp Ile Phe Cys Phe His Leu Lys Ser Trp Lys Ser Ser Arg Ile
50 55 60
Phe Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Ile Ile Cys Leu
65 70 75 80
Pro Phe Leu Met Asp Asn Tyr Val Arg Arg Trp Asp Trp Lys Phe Gly
85 90 95
Asp Ile Pro Cys Arg Leu Met Leu Phe Met Leu Ala Met Asn Arg Gln
100 105 110

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Gly Ser Ile Ile Phe Leu Thr Val Val Ala Val Asp Arg Tyr Phe Arg
115 120 125
Val Val His Pro His His Ala Leu Asn Lys Ile Ser Asn Arg Thr Ala
130 135 140
Ala Ile Ile Ser Cys Leu Leu Trp Gly Ile Thr Ile Gly Leu Thr Val
145 150 155
His Leu Leu Lys Lys Leu Met Pro Ile Gln Asn Gly Gly Ala Asn Leu
160 165 170
Cys Ser Ser Phe Ser Ile Cys His Thr Phe Gln Trp His Glu Ala Met
180 185 190
Phe Leu Leu Glu Phe Phe Leu Pro Leu Gly Ile Ile Leu Phe Cys Ser
195 200 205
Ala Arg Ile Ile Trp Ser Leu Arg Gln Arg Gln Met Asp Arg His Ala
210 215 220
Lys Ile Lys Arg Ala Ile Thr Phe Ile Met Val Val Ala Ile Val Phe
225 230 235
Val Ile Cys Phe Leu Pro Ser Val Val Val Arg Ile Arg Ile Phe Trp
240 245 250
Leu Leu His Thr Ser Gly Thr Gln Asn Cys Glu Val Tyr Arg Ser Val
255 260 265
Asp Leu Ala Phe Phe Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
270 275 280
Leu Asp Pro Val Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Asn Phe
285 290 295
Phe Ser Thr Leu Ile Asn Arg Cys Leu Gln Arg Lys Met Thr Gly Glu
300 305 310
Pro Asp Asn Asn Arg Ser Thr Ser Val Glu Leu Thr Gly Asp Pro Asn
315 320 325
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ctctccaca tptctatctt ctcaccagcg ctgggtgctt ggcagctgg cgcctggcc 360

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Cys Cys Phe Pro Thr Phe Leu Ile Trp Leu Ser Lys Trp Gln Asp Ala
180 185 190
Gln Leu Glu Glu Gln Gly Ala Ser Tyr Ile Leu Pro Pro Ser Met Gly
195 200 205
Thr Gln Pro Gly Cys Gly Leu Leu Val Ile Val Thr Tyr Thr Ser Ile
210 215 220
Leu Cys Val Leu Phe Leu Cys Thr Ala Leu Ile Ala Asn Cys Phe Trp
225 230 235
Arg Ile Tyr Ala Glu Ala Lys Thr Ser Gly Ile Trp Gly Gln Gly Tyr
240 245 250
Ser Arg Ala Arg Gly Thr Leu Leu Ile His Ser Val Leu Ile Thr Leu
255 260 265
Tyr Val Ser Thr Gly Val Val Phe Ser Leu Asp Met Val Leu Thr Arg
270 275 280
Tyr His His Ile Asp Ser Gly Thr His Thr Trp Leu Leu Ala Asn
285 290 295
Ser Glu Val Leu Met Met Leu Pro Arg Ala Met Leu Pro Tyr Leu Tyr
300 305 310
Leu Leu Arg Tyr Arg Gln Leu Leu Gly Met Val Arg Gly His Leu Pro
315 320 325
Ser Arg Arg His Gln Ala Ile Phe Thr Ile Ser
330 335 340

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<213> Homo sapiens

<400> 39
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ttatgtata ctgggagat gtatcacag aataagagt ccagatgctt caatccagtt 720
gtacacaaac agagagtgat gaattgaca aagatgtgc ttgtctggtt ggtgctttt 780

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gccattgtgc ttgcacacca cctggcagtc atccatcac tgcctactt cctcttctg 480
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<210> 38
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<213> Homo sapiens

<400> 38
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35 40 45
Leu Tyr Trp Leu Phe Leu Pro Ser Ser Leu Leu Ala Ala Thr Leu
50 55 60
Ala Val Ser Pro Leu Leu Val Thr Ile Leu Arg Asn Gln Arg Leu
65 70 75 80
Arg Gln Glu Pro His Tyr Leu Leu Pro Ala Asn Ile Leu Leu Ser Asp
85 90 95
Leu Ala Tyr Ile Leu Leu His Met Leu Ile Ser Ser Ser Ser Leu Gly
100 105 110
Gly Trp Glu Leu Gly Arg Met Ala Cys Gly Ile Leu Thr Asp Ala Val
115 120 125
Phe Ala Ala Cys Thr Ser Thr Ile Leu Ser Phe Thr Ala Ile Val Leu
130 135 140
His Thr Tyr Leu Ala Val Ile His Pro Leu Arg Tyr Leu Ser Phe Met
145 150 155
Ser His Gly Ala Ala Trp Lys Ala Val Ala Leu Ile Trp Leu Val Ala
160 165 170 175

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acctggcct tctatggg ttattactt tcatctgtc tcaactatg cagcagcagc 900
ataacacct ttctctatc cctgagtg ggaatttcc ggaactgct gcttcaatt 960
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tag 1023

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35 40 45
Leu Val Gly Asn Ile Leu Ile Val Phe Thr Ile Arg Ser Arg Lys
50 55 60
Lys Thr Val Pro Asp Ile Tyr Ile Cys Asn Leu Ala Val Ala Asp Leu
65 70 75 80
Val His Ile Val Gly Met Pro Phe Leu Ile His Gln Trp Ala Arg Gly
85 90 95
Gly Glu Trp Val Phe Gly Gly Pro Leu Cys Thr Ile Ile Thr Ser Leu
100 105 110
Asp Thr Cys Asn Gln Phe Ala Cys Ser Ala Ile Met Thr Met Ser
115 120 125
Val Asp Arg Tyr Phe Ala Leu Val Gln Pro Phe Arg Thr Thr Arg Trp
130 135 140
Arg Thr Arg Tyr Lys Thr Ile Arg Ile Asn Leu Gly Leu Trp Ala Ala
145 150 155
Ser Phe Ile Leu Ala Leu Pro Val Trp Val Tyr Ser Lys Val Ile Lys
160 165 170 175
Phe Lys Asp Gly Val Glu Ser Cys Ala Phe Asp Leu Thr Ser Pro Asp
180 185 190
Asp Val Leu Trp Tyr Thr Leu Tyr Leu Thr Ile Thr Thr Phe Phe
195 200 205
Pro Leu Pro Leu Ile Leu Val Cys Tyr Ile Leu Ile Leu Cys Tyr Thr
210 215 220
Trp Glu Met Tyr Gln Gln Asn Lys Asp Ala Arg Cys Cys Asn Pro Ser
225 230 235 240
Val Pro Lys Gln Arg Val Met Lys Leu Thr Lys Met Val Leu Val Leu

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243 250 255
Val Val Val Phe Ile Leu Ser Ala Ala Pro Tyr His Val Ile Gln Leu
260 265 270
Val Asn Leu Gln Met Glu Gln Pro Thr Leu Ala Phe Tyr Val Gly Tyr
275 280 285
Tyr Leu Ser Ile Cys Leu Ser Tyr Ala Ser Ser Ser Ile Asn Pro Phe
290 295 300
Leu Tyr Ile Leu Leu Ser Gly Asn Phe Gln Lys Arg Leu Pro Gln Ile
305 310 315 320
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Lys Ser His Phe
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<210> 44
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Page 40

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<400> 44
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<400> 46
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Page 42

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<400> 68
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<400> 71
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<210> 72

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<400> 75
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<210> 77

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<211> 24
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24

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<210> 81
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<210> 83
<211> 1356
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Glu Val Gly Leu Arg Asp Val Ala Ser Glu Ser Val Ala Leu Phe Phe
35 40 45

Met Leu Leu Leu Asp Leu Thr Ala Val Ala Gly Asn Ala Ala Val Met
50 55 60

Ala Val Ile Ala Lys Thr Pro Ala Leu Arg Lys Phe Val Phe Val Phe
65 70 75 80

His Leu Cys Leu Val Asp Leu Leu Ala Ala Leu Thr Leu Met Pro Leu
85 90 95

Ala Met Leu Ser Ser Ser Ala Leu Phe Asp His Ala Leu Phe Gly Glu
100 105 110

Val Ala Cys Arg Leu Tyr Leu Phe Leu Ser Val Cys Phe Val Ser Leu
115 120 125

Ala Ile Leu Ser Val Ser Ala Ile Asn Val Glu Arg Tyr Tyr Val
130 135 140

Val His Pro Met Arg Tyr Glu Val Arg Met Thr Leu Gly Leu Val Ala
145 150 155 160

Ser Val Leu Val Gly Val Trp Val Lys Ala Leu Ala Met Ala Ser Val
165 170 175

Pro Val Leu Gly Arg Val Ser Trp Glu Glu Gly Ala Pro Ser Val Pro
180 185 190

Pro Gly Cys Ser Leu Gln Trp Ser His Ser Ala Tyr Cys Gln Leu Phe
195 200 205

Val Val Val Phe Ala Val Leu Tyr Phe Leu Leu Pro Leu Leu Ile
210 215 220

Leu Val Val Tyr Cys Ser Met Phe Arg Val Ala Arg Val Ala Met
225 230 235 240

Gln His Gly Pro Leu Pro Thr Trp Met Glu Thr Pro Arg Gln Arg Ser
245 250 255

Glu Ser Leu Ser Ser Arg Ser Thr Met Val Thr Ser Ser Gly Ala Pro
260 265 270

Gln Thr Thr Pro His Arg Thr Phe Gly Gly Gly Lys Ala Val Val
275 280 285

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275 280 285
Leu Leu Ala Val Gly Gly Gln Phe Leu Leu Cys Trp Leu Pro Tyr Phe
290 295 300
Ser Phe His Leu Tyr Val Ala Leu Ser Ala Gln Pro Ile Ser Thr Gly
305 310 315 320
Gln Val Glu Ser Val Val Thr Trp Ile Gly Tyr Phe Cys Phe Thr Ser
325 330 335
Asn Pro Phe Thr Tyr Gly Cys Leu Asn Arg Gln Ile Arg Gly Glu Leu
340 345 350
Ser Lys Gln Phe Val Cys Phe Phe Lys Pro Ala Pro Glu Glu Leu
355 360 365
Arg Leu Pro Ser Arg Glu Gly Ser Ile Glu Glu Asn Phe Leu Gln Phe
370 375 380
Leu Gln Gly Thr Gly Cys Pro Ser Glu Ser Trp Val Ser Arg Pro Leu
385 390 395 400
Pro Ser Pro Lys Gln Glu Pro Pro Ala Val Asp Phe Arg Ile Pro Gly
405 410 415
Gln Ile Ala Glu Glu Thr Ser Glu Phe Leu Glu Gln Gln Thr Ser
420 425 430
Asp Ile Ile Met Ser Asp Ser Tyr Leu Arg Pro Ala Ala Ser Pro Arg
435 440 445
Leu Glu Ser
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<210> 85
<211> 28
<212> DNA
<213> Homo sapiens

<400> 85
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28

<210> 86
<211> 28
<212> DNA
<213> Homo sapiens

<400> 86
gatgatgtgt gtggtctttg ccttcttg

28

<210> 87
<211> 1041
<212> DNA
<213> Homo sapiens

<400> 87
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ttcccaattg tatatctgat aatttttttc tgggaagctt tgggaattg gttgtccata

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1atgttttcc tgcagcctta taagaagtc acatctgtga agcttttcat gctaaattctg 240
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aacatgtaca gcagttatita tttcttgacc gtgtgtgagt ttgtgtgttt ccttgcaagt 420
gttcaacctt ttggtcttct gcatgtccac agcaccagga gtctctgagt cctctgtggg 480
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gacagactgc ataaagcttt ggtatcaca ctggcttggg cagcagcaca tgcctgtctc 900
aatctctgtc tctattactt tctgtggggg aattttaag acagactaaa gtctgcactc 960
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<210> 88
<211> 346
<212> PRT
<213> Homo sapiens

<400> 88

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35 40 45
Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu
50 55 60
Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu
65 70 75 80
Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp
85 90 95
Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg
100 105 110
Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe
115 120 125
Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe
130 135 140

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Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly
145 150 155 160
Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser
165 170 175
Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu
180 185 190
Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val
195 200 205
Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile
210 215 220
Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val
225 230 235 240
Ser His Arg Lys Ala Lys Thr Thr Ile Ile Thr Leu Ile Ile Phe
245 250 255
Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr
260 265 270
Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Ala Leu Val
275 280 285
Ile Thr Leu Ala Leu Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu
290 295 300
Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu
305 310 315 320
Arg Lys Gly His Pro Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val
325 330 335
Ser Val Trp Leu Arg Lys Glu Thr Arg Val
340 345

<210> 89
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<212> DNA
<213> Artificial Sequence

<220>
<221> misc feature
<223> Novel Sequence

<400> 89
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<210> 90
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<221> misc feature
<223> Novel Sequence

<400> 90
gaagtcact tctttagctt tgcactgg

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28

<210> 91
<211> 1527
<212> DNA
<213> Homo sapiens

<400> 91

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cagctgtgac agtgacaaa cgtttttacc tttaacctcc tctgacaga cctgtgtcag 240
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accattgtgc tgggttcagt ggtatctatc tgttccatca tccacctctc ctctactccg 420
tccaaagatg cccagcggcg cgtttactgt ctctctatag gaaactggat tctgtccatc 480
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aggcagcatg ctctgtgta caattctcag apacacagct tggaaagtcg agtcaagpac 720
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atctctctca tctatttct ctatgtgta tctctgggg cctactgctt tttagagtc 1260
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tctactgatt ctgtacttct tcttga 1527

<210> 92
<211> 508
<212> PRT
<213> Homo sapiens

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<400> 92

Met Thr Ser Thr Cys Thr Asn Ser Thr Arg Glu Ser Asn Ser Ser His
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Thr Cys Met Pro Leu Ser Lys Met Pro Ile Ser Leu Ala His Gly Ile
20 25 30
Ile Arg Ser Thr Val Leu Val Ile Phe Leu Ala Ala Ser Phe Val Gly
35 40 45
Asn Ile Val Leu Ala Leu Val Leu Gln Arg Lys Pro Gln Leu Leu Gln
50 55 60
Val Thr Asn Arg Phe Ile Phe Asn Leu Leu Val Thr Asp Leu Leu Gln
65 70 75 80
Ile Ser Leu Val Ala Pro Trp Val Val Ala Thr Ser Val Pro Phe
85 90 95
Trp Pro Leu Asn Ser His Phe Cys Thr Ala Leu Val Ser Leu Thr His
100 105 110
Leu Phe Ala Phe Ala Ser Val Asn Thr Ile Val Val Ser Val Asp
115 120 125
Arg Tyr Leu Ser Ile Ile His Pro Leu Ser Tyr Pro Ser Lys Met Thr
130 135 140
Gln Arg Arg Gly Tyr Leu Leu Tyr Gly Thr Trp Ile Val Ala Ile
145 150 155 160
Leu Gln Ser Thr Pro Pro Leu Tyr Gly Trp Gly Gln Ala Ala Phe Asp
165 170 175
Glu Arg Asn Ala Leu Cys Ser Met Ile Trp Gly Ala Ser Pro Ser Tyr
180 185 190
Thr Ile Leu Ser Val Val Ser Phe Ile Val Ile Pro Leu Ile Val Met
195 200 205
Ile Ala Cys Tyr Ser Val Val Phe Cys Ala Ala Arg Gln His Ala
210 215 220
Leu Leu Tyr Asn Val Lys Arg His Ser Leu Gln Val Arg Val Lys Asp
225 230 235 240
Cys Val Glu Asn Glu Asp Glu Glu Gly Ala Glu Lys Lys Glu Glu Phe
245 250 255
Gln Asp Glu Ser Glu Phe Arg Arg Gln His Glu Gly Glu Lys Ala
260 265 270
Lys Glu Gly Arg Met Glu Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu
275 280 285
Gly Ser Thr Gly Thr Ser Glu Ser Ser Val Glu Ala Arg Gly Ser Glu
290 295 300
Glu Val Arg Glu Ser Ser Thr Val Ala Ser Asp Gly Ser Met Glu Gly
305 310 315 320
Lys Glu Gly Ser Thr Lys Val Glu Glu Asn Ser Met Lys Ala Asp Lys
325 330 335

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Gly Arg Thr Glu Val Asn Gln Cys Ser Ile Asp Leu Gly Glu Asp Asp
340 345 350
Met Glu Phe Gly Glu Asp Asp Ile Asn Phe Ser Glu Asp Asp Val Glu
355 360 365
Ala Val Asn Ile Pro Glu Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn
370 375 380
Ser Asn Pro Pro Leu Pro Arg Cys Tyr Gln Cys Lys Ala Lys Lys Val
385 390 395 400
Ile Phe Ile Ile Ile Phe Ser Tyr Val Leu Ser Leu Gly Pro Tyr Cys
405 410 415
Phe Leu Ala Val Leu Ala Val Trp Val Asp Val Glu Thr Gln Val Pro
420 425 430
Gln Trp Val Ile Thr Ile Ile Ile Trp Leu Phe Phe Leu Gln Cys Cys
435 440 445
Ile His Pro Tyr Val Tyr Gly Tyr Met His Lys Thr Ile Lys Lys Glu
450 455 460
Ile Gln Asp Met Leu Lys Lys Phe Phe Cys Lys Glu Lys Pro Pro Lys
465 470 475 480
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485 490 495
Lys Ile Val Pro Ser Tyr Asp Ser Ala Thr Phe Pro
500 505

<210> 93
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<212> DNA
<213> Artificial Sequence
<220>
<221> misc_feature
<223> Novel Sequence

<400> 93
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<210> 94
<211> 29
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_feature
<223> Novel Sequence

<400> 94
gcacatttc cttctggcc ggtggcc

29

<210> 95
<211> 1092
<212> DNA

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<213> Homo sapiens

<400> 95
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tcagcgtcc tctgtgtaa tctgtcgtg ggcacctgc tctgtgccc gctgacatg 180
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tctgtgccc tctgtgccc cgtgtgccc cgtgtgccc agcgcacgc cgcgcacgc 960
tcacacacg agcgcacgc ggtgtgccc gctgtgccc agcgcacgc gtagcgcgc 1020
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cgcgcacgc ga 1092

<210> 96
<211> 363
<212> PRT
<213> Homo sapiens

<400> 96
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20 25 30
Ser Ala Glu Leu Arg Thr Arg Ala Ser Gly Val Leu Leu Val Asn Leu
35 40 45
Ser Leu Gly His Leu Leu Leu Ala Leu Asp Met Pro Phe Thr Leu
50 55 60
Leu Gly Val Met Arg Gly Arg Thr Pro Ser Ala Pro Gly Ala Cys Gln
65 70 75 80
Val Ile Gly Phe Leu Asp Thr Phe Leu Ala Ser Asn Ala Leu Ser
Page 57

85 90 95
Val Ala Ala Leu Ser Ala Asp Gln Trp Leu Ala Val Gly Glu Pro Leu
100 105 110
Arg Tyr Ala Gly Arg Leu Arg Pro Arg Tyr Ala Gly Leu Leu Gly
115 120 125
Cys Ala Trp Gly Gln Ser Leu Ala Phe Ser Gly Ala Ala Leu Gly Cys
130 135 140
Ser Trp Leu Gly Tyr Ser Ser Ala Phe Ala Ser Cys Ser Leu Arg Leu
145 150 155 160
Pro Pro Glu Pro Glu Arg Pro Arg Phe Ala Phe Thr Ala Thr Leu
165 170 175
His Ala Val Gly Phe Val Leu Pro Leu Ala Val Leu Cys Leu Thr Ser
180 185 190
Leu Gln Val His Arg Val Ala Arg Ser His Cys Gln Arg Met Asp Thr
195 200 205
Val Thr Met Lys Ala Leu Ala Leu Ala Asp Leu His Pro Ser Val
210 215 220
Arg Gln Arg Cys Leu Ile Gln Gln Lys Arg Arg His Arg Ala Thr
225 230 235 240
Arg Lys Ile Gly Ile Ala Ile Ala Thr Phe Leu Ile Cys Phe Ala Pro
245 250 255
Tyr Val Met Thr Arg Leu Ala Gln Leu Val Pro Phe Val Thr Val Asn
260 265 270
Ala Gln Lys Gly Ile Leu Ser Lys Cys Leu Thr Tyr Ser Lys Ala Val
275 280 285
Ala Asp Pro Phe Thr Tyr Ser Leu Leu Arg Arg Pro Phe Arg Gln Val
290 295 300
Leu Ala Gly Met Val His Arg Leu Lys Lys Arg Thr Pro Arg Pro Ala
305 310 315 320
Ser Thr His Asp Ser Ser Leu Asp Val Ala Gly Met Val His Gln Leu
325 330 335
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Thr Gln Asn Asp Ser Cys Leu Gln Gln Thr His
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<210> 97
<211> 34
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_feature
<223> Novel Sequence

<400> 97
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34

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<210> 98
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Novel Sequence

<400> 98
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<210> 99
<211> 2610
<212> DNA
<213> Homo sapiens and Rat

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gagactctt agtcttga cagcagct cactgacga tcatctgt agcagctac 1320

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ctccgtcttg ccgctctacc ccgctctgag taccgataat ctgcagatt ccaactacat 1380
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<210> 100
 <211> 869
 <212> PRT
 <213> Homo sapiens and Rat

<400> 100

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 20 25 30
 Glu Val Gly Leu Arg Asp Val Ala Ser Glu Ser Val Ala Leu Phe Phe
 35 40 45
 Met Leu Leu Asp Leu Thr Ala Val Ala Gly Asn Ala Ala Val Met
 50 55 60

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Ala Val Ile Ala Lys Thr Pro Ala Leu Arg Lys Phe Val Phe Val Phe
 65 70 75 80
 His Leu Cys Leu Val Asp Leu Leu Ala Ala Leu Thr Leu Met Pro Leu
 85 90 95
 Ala Met Leu Ser Ser Ser Ala Leu Phe Asp His Ala Leu Phe Gly Glu
 100 105 110
 Val Ala Cys Arg Leu Tyr Leu Phe Leu Ser Val Cys Phe Val Ser Leu
 115 120 125
 Ala Ile Leu Ser Val Ser Ala Ile Asn Val Glu Arg Tyr Tyr Val
 130 135 140
 Val His Pro Met Arg Tyr Glu Val Arg Met Thr Leu Gly Leu Val Ala
 145 150 155 160
 Ser Val Leu Val Gly Val Trp Val Lys Ala Leu Ala Met Ala Ser Val
 165 170 175
 Pro Val Leu Gly Arg Val Ser Trp Glu Glu Gly Ala Pro Ser Val Pro
 180 185 190
 Pro Gly Cys Ser Leu Gln Trp Ser His Ser Ala Tyr Cys Gln Leu Phe
 195 200 205
 Val Val Val Phe Ala Val Leu Tyr Phe Leu Leu Pro Leu Leu Ile
 210 215 220
 Leu Val Val Tyr Cys Ser Met Phe Arg Val Ala Arg Val Ala Ala Met
 225 230 235 240
 Gln His Gly Pro Leu Pro Thr Trp Met Gln Thr Pro Arg Gln Arg Ser
 245 250 255
 Glu Ser Leu Ser Ser Arg Ser Thr Met Val Thr Ser Ser Gly Ala Pro
 260 265 270
 Gln Thr Thr Pro His Arg Thr Phe Gly Gly Lys Ala Val Val
 275 280 285
 Leu Leu Ala Val Gly Gly Glu Phe Leu Leu Cys Trp Leu Pro Tyr Phe
 290 295 300
 Ser Phe His Leu Tyr Val Ala Leu Ser Ala Gln Pro Ile Ser Thr Gly
 305 310 315 320
 Gln Val Glu Ser Val Val Thr Trp Ile Gly Tyr Phe Cys Phe Thr Ser
 325 330 335
 Asn Pro Phe Phe Tyr Gly Cys Leu Asn Arg Gln Ile Arg Gly Glu Leu
 340 345 350
 Ser Lys Gln Phe Val Cys Phe Phe Lys Pro Ala Pro Glu Glu Leu
 355 360 365
 Arg Leu Pro Ser Arg Glu Gly Ser Ile Glu Glu Asn Phe Leu Gln Phe
 370 375 380
 Leu Gln Gly Thr Gly Cys Pro Ser Glu Ser Trp Val Ser Arg Pro Leu
 385 390 395 400
 Pro Ser Pro Lys Gln Glu Pro Pro Ala Val Asp Phe Arg Ile Pro Gly
 405 410 415

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Gln Ile Ala Glu Glu Thr Ser Glu Phe Leu Glu Gln Leu Thr Ser
 420 425 430
 Asp Ile Ile Met Ser Asp Ser Tyr Leu Arg Pro Ala Ala Ser Pro Arg
 435 440 445
 Leu Glu Ser Ala Ile Ser Ala Glu Phe His Ile Thr Gly Leu Val Asp
 450 455 460
 Pro Ser Ser Val Pro Ser Leu Gly Cys Arg Ser Met Gly Cys Leu Gly
 465 470 475 480
 Asn Ser Lys Thr Glu Asp Gln Arg Asn Glu Glu Lys Ala Gln Arg Glu
 485 490 495
 Ala Asn Lys Lys Ile Glu Lys Gln Leu Gln Lys Asp Lys Gln Val Tyr
 500 505 510
 Arg Ala Thr His Arg Leu Leu Leu Leu Gly Ala Gly Ser Gly Lys
 515 520 525
 Ser Thr Ile Val Lys Gln Met Arg Ile Leu His Val Asn Gly Phe Asn
 530 535 540
 Gly Glu Gly Gly Glu Glu Asp Pro Gln Ala Ala Arg Ser Asn Ser Asp
 545 550 555 560
 Gly Glu Lys Ala Thr Lys Val Gln Asp Ile Lys Asn Asn Leu Lys Glu
 565 570 575
 Ala Ile Glu Thr Ile Val Ala Ala Met Ser Asn Leu Val Pro Val
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(25) Filing Language: English (72) Inventors and (75) Inventors/Applicants (for US only): CHEN, Rongping (CN/US); 5296 Timber Branch Way, San Diego, CA 92130 (US); DANG, Hwang, T. [US/US]; 5352 Oak Park Drive, San Diego, CA 92105 (US); LOWITZ, Kevin, P. [US/US]; 8031 Camino de Piza #C, San Diego, CA 92108 (US).

(26) Publication Language: English (74) Agents: MILLER, Suzanne, E. et al.; Woodcock Washburn Kertz MacKiewicz & Norris LLP, One Liberty Place - 46th Floor, Philadelphia, PA 19103 (US).

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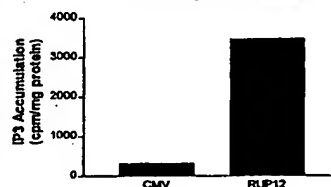
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[Continued on next page]

(54) Title: ENDOGENOUS AND NON-ENDOGENOUS VERSIONS OF HUMAN G PROTEIN-COUPLED RECEPTORS

IP3 Assay in 293 Cells



(57) Abstract: The invention disclosed in this patent document relates to transmembrane receptors, more particularly to a human G protein-coupled receptor for which the endogenous ligand is unknown ("orphan GPCR receptor"), and most particularly to sustained (non-endogenous) versions of the human GPCRs for evidence of constitutive activity.

INTERNATIONAL SEARCH REPORT

PCT/US 00/31509

Category	Claims of document, with indication, where appropriate, of the relevant passages	Relevant to claim no.
P,X	DATABASE EMBL 'Online! AC: A8038237, 4 May 2000 (2000-05-04) OHONO ET AL.: "Homo sapiens mRNA for G protein-coupled receptor C5L2, complete cds" XP002175947 abstract	9-12
P,X	WO 00 14229 A (ONO MITSUOKU; KANO KIMIYOSHI (JP); ASAHI CHEMICAL IND (JP); ISHII) 16 March 2000 (2000-03-16) page 98 -page 101; claim 4 page 103; claim 5	9-12
E	WO 01 36471 A (ARENA PHARMACEUTICALS INC.; CHEN RUOPING (US); DANG HUONG T (US); L) 25 May 2001 (2001-05-25) Seq. Id. No. 3 (claims 5-8) Seq. Id. No. 5 (claims 9-12) Seq. Id. No. 7 (claims 13-16) Seq. Id. No. 9 (claims 17-20) Seq. Id. No. 11 (claims 21-24) Seq. Id. No. 13 (claims 25-28) Seq. Id. No. 21 (claims 41-44) Seq. Id. No. 19, 23 (claims 45-48) Seq. Id. No. 25 (claims 49-52)	5-28, 41-52
E	EP 1 094 076 A (PFIZER LTD; PFIZER (US)) 25 April 2001 (2001-04-25) Seq. Id. No. 1	9-12
E	WO 01 31014 A (UPJOHN CO; VOGELI GABRIEL (US); WOOD LINDA S (US); MERCHANT KALPAN) 3 May 2001 (2001-05-03) Sequence No. 5	13-16
X	PATENT ABSTRACTS OF JAPAN vol. 1999, no. 09, 30 July 1999 (1999-07-30) & JP 11 098988 A (SMITHKLINE BEECHAM CORP.), 13 April 1999 (1999-04-13) abstract & DATABASE EMBL 'Online! AC: E31720; E75225, 22 February 2001 (2001-02-22) JEFFREY L.M.D.D. AND BERESNA V.S.H.H.: "cDNA clone Hcald54 encoding human seven-pass transmembrane receptor" abstract	13-16
X	US 5 955 308 A (BERESNA DERK J ET AL) 21 September 1999 (1999-09-21) Sequence 1	13-16

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PCT/US 00/31509

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A	page 55 -page 56; claim 25	17-20, 57-60
X	page 52 -page 54; claim 21	37-40
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A	DATABASE EMBL 'Online! AC: AL065769, 20 May 1999 (1999-05-29) GENSCFIDE: "Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RPI1-98 library from Drosophila melanogaster (fruit fly)" XP002175910 abstract	49-52
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E	WO 01 12673 A (MERCK PATENT GMBH ;DUECKER KLAUS (DE)) 22 February 2001 (2001-02-22) Sequence 1, 2 page 39; claim 3	61-64
X	JP 11 032770 A (ASAHI CHEM IND CO LTD) 9 February 1999 (1999-02-09) page 19; claim 7	65-68
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C. (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 00/31509

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:

see additional sheet

1. ☒ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claim No.:

Remarks on Prior Art

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

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International Application No. PCT/US 00/31509

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-4
6 protein-coupled receptor as characterized by SEQ.ID.2, its non-endogenous, constitutively activated version, a cDNA encoding said receptor as characterized by SEQ.ID.1, a plasmid comprising said cDNA, and a host cell comprising said plasmid.
2. Claims: 5-8
6 protein-coupled receptor as characterized by SEQ.ID.4, its non-endogenous, constitutively activated version, a cDNA encoding said receptor as characterized by SEQ.ID.3, a plasmid comprising said cDNA, and a host cell comprising said plasmid.
3. Claims: 9-12
6 protein-coupled receptor as characterized by SEQ.ID.6, its non-endogenous, constitutively activated version, a cDNA encoding said receptor as characterized by SEQ.ID.5, a plasmid comprising said cDNA, and a host cell comprising said plasmid.
4. Claims: 13-16
6 protein-coupled receptor as characterized by SEQ.ID.8, its non-endogenous, constitutively activated version, a cDNA encoding said receptor as characterized by SEQ.ID.7, a plasmid comprising said cDNA, and a host cell comprising said plasmid.
5. Claims: 17-20
6 protein-coupled receptor as characterized by SEQ.ID.10, its non-endogenous, constitutively activated version, a cDNA encoding said receptor as characterized by SEQ.ID.9, a plasmid comprising said cDNA, and a host cell comprising said plasmid.
6. Claims: 21-24
6 protein-coupled receptor as characterized by SEQ.ID.12, its non-endogenous, constitutively activated version SEQ.ID.11, a cDNA encoding said receptor as characterized by SEQ.ID.11, a plasmid comprising said cDNA, and a host cell comprising said plasmid.

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FURTHER INFORMATION CONTINUED FROM PCT/AS/ 210

7. Claims: 25-28

6 protein-coupled receptor as characterized by SEQ.ID.14, its non-endogenous, constitutively activated version SEQ.ID. 88, a cDNA encoding said receptor as characterized by SEQ.ID.13, a plasmid comprising said cDNA, and a host cell comprising said plasmid.

8. Claims: 29-32

6 protein-coupled receptor as characterized by SEQ.ID.16, its non-endogenous, constitutively activated version SEQ.ID.92, a cDNA encoding said receptor as characterized by SEQ.ID.15, a plasmid comprising said cDNA, and a host cell comprising said plasmid.

9. Claims: 33-36

6 protein-coupled receptor as characterized by SEQ.ID.18, its non-endogenous, constitutively activated version, a cDNA encoding said receptor as characterized by SEQ.ID.17, a plasmid comprising said cDNA, and a host cell comprising said plasmid.

10. Claims: 37-40

6 protein-coupled receptor as characterized by SEQ.ID.20, its non-endogenous, constitutively activated version, a cDNA encoding said receptor as characterized by SEQ.ID.19, a plasmid comprising said cDNA, and a host cell comprising said plasmid.

11. Claims: 41-44

6 protein-coupled receptor as characterized by SEQ.ID.22, its non-endogenous, constitutively activated version, a cDNA encoding said receptor as characterized by SEQ.ID.21, a plasmid comprising said cDNA, and a host cell comprising said plasmid.

12. Claims: 45-48

6 protein-coupled receptor as characterized by SEQ.ID.24, its non-endogenous, constitutively activated version, a cDNA encoding said receptor as characterized by SEQ.ID.23, a plasmid comprising said cDNA, and a host cell comprising said plasmid.

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FURTHER INFORMATION CONTINUED FROM PCT/AS/ 210

13. Claims: 49-52

6 protein-coupled receptor as characterized by SEQ.ID.26, its non-endogenous, constitutively activated version, a cDNA encoding said receptor as characterized by SEQ.ID.25, a plasmid comprising said cDNA, and a host cell comprising said plasmid.

14. Claims: 53-56

6 protein-coupled receptor as characterized by SEQ.ID.28, its non-endogenous, constitutively activated version, a cDNA encoding said receptor as characterized by SEQ.ID.27, a plasmid comprising said cDNA, and a host cell comprising said plasmid.

15. Claims: 57-60

6 protein-coupled receptor as characterized by SEQ.ID.30, its non-endogenous, constitutively activated version, a cDNA encoding said receptor as characterized by SEQ.ID.29, a plasmid comprising said cDNA, and a host cell comprising said plasmid.

16. Claims: 61-64

6 protein-coupled receptor as characterized by SEQ.ID.32, its non-endogenous, constitutively activated version, a cDNA encoding said receptor as characterized by SEQ.ID.31, a plasmid comprising said cDNA, and a host cell comprising said plasmid.

17. Claims: 65-68

6 protein-coupled receptor as characterized by SEQ.ID.34, its non-endogenous, constitutively activated version, a cDNA encoding said receptor as characterized by SEQ.ID.33, a plasmid comprising said cDNA, and a host cell comprising said plasmid.

18. Claims: 69-72

6 protein-coupled receptor as characterized by SEQ.ID.36, its non-endogenous, constitutively activated version, a cDNA encoding said receptor as characterized by SEQ.ID.35, a plasmid comprising said cDNA, and a host cell comprising said plasmid.

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FURTHER INFORMATION CONTINUED FROM PCT/AS/ 210

19. Claims: 73-76

6 protein-coupled receptor as characterized by SEQ.ID.38, its non-endogenous, constitutively activated version, a cDNA encoding said receptor as characterized by SEQ.ID.37, a plasmid comprising said cDNA, and a host cell comprising said plasmid.

20. Claims: 77-80

6 protein-coupled receptor as characterized by SEQ.ID.40, its non-endogenous, constitutively activated version, a cDNA encoding said receptor as characterized by SEQ.ID.39, a plasmid comprising said cDNA, and a host cell comprising said plasmid.

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